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Title:
Perfect score:
Sequence:
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Maximum
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1: /cgn2_6/ptodata/;
2: /cgn2_6/ptodata/;
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4: /cgn2_6/ptodata/;
5: /cgn2_6/ptodata/
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
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PCT-US95-04681-21
US-08-673-789-4
US-08-673-789-3
US-08-673-789-3
US-08-673-789-3
US-08-673-789-3
US-08-702-367A-15
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Result No.

ALIGNMENTS

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TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
TYPE: amino acids
TYPE: honear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: PK6841 (AU)
FILING DATE: 21-JUN-1991
PRIOR APPLICATION UNMBER: PK9992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION NUMBER: PCT/AU92/00294
APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DIGITION STATE

APPLICATION PAPELORIUM:
APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                               NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9159
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Boyd, Andrew W. APPLICANT: Simpson, Richar APPLICANT: Wicks, Ian APPLICANT: Ward, Larry D. APPLICANT: Wilkinson, Davi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE TITLE OF INVENTION: AND USE THEREOF NUMBER OF SEQUENCES: 14
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CURRENT APPLICATION DATA:
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FILING DATE: 18-APR-1994
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5. 5674691
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T: 400 Garden City Plaza
Garden City
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                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21, Application US/08449645A
Patent No. 5981245
GENERAL INFORMATION:
                                                                          Query Match
Best Local Similarity
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Best Local
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION: EPH-LIKE
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
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STATE: California
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MDCQLSILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDE
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Pred. No. 5.2
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Pred. No. 5.2e-146;
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5.2e-146;
95 0;
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Best Local S
Matches 271
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APPLICANT: Fox, G
                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOCOMPATION:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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STATE: California
                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 1: MOLECULE TYPE:
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LENGTH: 983 amino acid
TYPE: amino acid
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: EPH-Like
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                        1 MDCQLSILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDE 60
                                                                                             HTTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETF
                                                                                                                HYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETF 120
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LAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCVNNSKEEDPP
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Pred. No. 5.2e-146;
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                                                                           Matches
                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                  -08-715-106-10
                                                                                                                                                                                                                                              TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 20 901 SANS UR
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    AFFILMS DATE: 19-JUN-13-2
FILING DATE: 19-JUN-13-2
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGIO, Frank S.
NAME: DIGIGIO, Frank S.
NAME: 0164910, Frank S.
NAME: 0164910, Frank S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,919
FILING DATE: 18-APR-1994
APPLICATION NUMBER: PK6841 (AU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE
TITLE OF INVENTION: AND USE THEREOF
                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 9159
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEPAX: (516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT//
FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 21-JUN-1991 PRIOR APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Boyd, Andrew W. APPLICANT: Simpson, Richard J. APPLICANT: Wicks, Ian
                                                              Local 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 400 Garden City Plaza CITY: Garden City STATE: New York
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ZIP: 11530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                     LENGTH:
MDCQLSILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDE 60
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                                                                        Score 1466; DB 3;
Pred. No. 5.2e-146;
; Mismatches 0;
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PCT-US95-04681-21
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                                                                                                                                                                                                                            Matches 271;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: EPH-Like
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 28
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181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Thousand Oaks
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                  1 MDCQLSILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDE 60
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Pred. No. 5.2e-146;
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US-08-162-809-16
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NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-LJ 9503

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9901

TELEPAX: (619) 535-9949

INFORMATION FOR SEQ ID NO: 16:

SEQUENCE CHARACTERISTICS:

LEWITH. 033 5545-5655
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 240; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 4370 La JOLLA
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,809
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS OF USE
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 514
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                                                                                                                                                                                EWLVPIGKCSCNAGYEERGFMCQ 271
                                                                             CVALVSVRVYFKKCPFTVKNLAMFDDTVPMDSQSLVEVRGSCVNNSKEEDPPRMYCSTEG
                                                                                                                                      DDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGA 188
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                                                          CVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCVNHSKEEEPPKMYCSTEG
                                                                                                                    DDHLAKFREHQFTKIDTMAADESFTQMDLGDRILKLNTEVREVGPVSKKGFYLAFQDVGA
EWLVPIGKCLCNAGYEERGFACQ
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Best Local S
Matches 240
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Patent No. 581447
                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 751-6849
TELEX: 421792
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPOTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,789
FILING DATE:
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/177
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: GEORGE, F. TITLE OF INVENTION: I
 248
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                                                                                                                                                                                                                                                                                                                                                                     TYPE: AMINO ACID
STRANDEDNESS: UNI
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                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                      CVALVSVRVYFKKCPFTVKNLAMFDDTVPMDSQSLVEVRGSCVNNSKEEDPPRMYCSTEG 248
EWLVPIGKCLCNAGYEERGFACQ 270
                         EWLVPIGKCSCNAGYEERGFMCQ 271
                                                    CVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCVNHSKEEEPPKMYCSTEG
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40; Conservative
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T.; KROMER, LAWRENCE, F.; VANDE WOUDE.
                                                                                                                                                                                                                                                                                                                                                          UNKNOWN
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TYROSINE KINASE AND LIGAND AND THEIR
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Pred. No. 1e-128;
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US-08-673-789-3
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APPLICANT: ZHOU, RENDING; SCHULZ, NI
APPLICANT: T; KROMER, LAWRENCE, F;
APPLICANT: GEORGE, F.
TITLE OF INVENTION: BSK RECEPTOR LIF
TITLE OF INVENTION: USE IN DIAGNOST:
TITLE OF INVENTION: METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/177,81:
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 751-6849
TELER: 421792
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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CORRESPONDENCE ADDRESS:
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TOPOLOGY: UNI
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/673,789
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                                                                                                             TIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPF 204
                                                                                                                                                                        EERGFMCQ
                                                                                                                                                                                                                                  PANEVTLLDSRSVQGELGWIASPLEGGWEEVSIMDEKNTPIRTYQVCNVMEASQNNWLRT 86
EERGFACQ 274
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                           271
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TYROSINE KINASE AND LIGAND AND THEIR
USE IN DIAGNOSTIC AND THERAPEUTIC
                                                                                                                                                                                                                                                                                            68.6%; Score 1005; DB 2; 73.0%; Pred. No. 2.2e-97; tive 33; Mismatches 32;
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                                                                                                                                                                                                                                                                                             32; Indels
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; TYPE: amino acid
; STRANDEDNESS: unkn
; TOPOLOGY: unknown
; MOLECULE TYPE: prote
US-08-469-537A-101
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GENERAL INFORMATION:
APPLICANT: MAISONDIETTE, et al.
TITLE OF INVENTION: EHK AND RC.
TITLE OF INVENTION: KINASES
TITLE OF STOULNCES: 107
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US-08-469-537A-101
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Best Local Similarity
Matches 180; Conservat
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Sequence 101, App...
Sequence 101, App...
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FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/406,247
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 08/144,992
FILING DATE: 28-OCT-1993
APPLICATION NUMBER: USSN 07/736,559
FILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Ph.D., Gail M
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG 070C
TELECHOME: 914-345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
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SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 948 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                 177
                                                                  173
232 NNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEE
                                                                                                                                  113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Regeneron Pharmaceuticals, STREET: 777 Old Saw Mill River Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                LGTCKETFTLYXIESDESHGTKFKPSQXIKIDTIAADESFTQMDLGDRILKLNTEVREVG
                               PIERKGFYLAFQDIGACIALVSVRVFYKKCPFTVRNLAMFPDTIPRVDSSSLVEVRGSCV
                                                  PVNKKGEYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCV 231
                                                                                                                              LGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVG 172
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                                                                                                                                                                                                                                                                                              68.4%; Score 1003; DB 2; 65.7%; Pred. No. 3.4e-97; tive 39; Mismatches 37;
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RESULT 11
US-08-702-367A-15
; Sequence 15, Application U;
; Sequence 15, Application U;
; Patent No. 5981246
; GENERAL INFORMATION:
; APPLICANT: FOX, GATY M
; TITLE OF INVENTION: EP;
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US-08-449-645A-15
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NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-2
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 986 amino acids
TYPE: amino acid
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Best Local Similarity
Matches 183; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FOX, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
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STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                             GACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPPRMYCS 245
                                                                                                                                                                                                                                                                                          SUNDKERFIRENGFVKIDTIAADESFTQVDIGDRIMKLNTEIRDVGPLSKKGFYLAFQDV
                                                                                                                                                                                                                                                                                                            SDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDV 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.9%; Score 995; DB 2; 68.8%; Pred. No. 2.5e-96;
EPH-Like Receptor Protein
                                                                       US/08702367A
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RESULT 12
PCT-US95-04681-15
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                                                                                                                                                                                                                             Sequence 15, Application PC/TUS9504681 GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1!
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,36
                                                                                                                                                                                           APPLICANT: FOX, Gary M.
TITLE OF INVENTION: EPH-Like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                          NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                      COUNTRY: U
ZIP: 91320
                                                                                     ADDRESSEE: Angen Patent Operations/RBW
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
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CLASSIFICATION: 435
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REFERENCE/DOCKET NUMBER: A-2
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 986 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 67.9%;
Best Local Similarity 68.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
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           COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb fl.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/222,616
FILING DATE: 4-APR.1994
                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                              APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
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CITY: South San Francisco
STATE: California
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SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                              ZIP: 94080
                                                                                                                                                          COUNTRY:
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CLASSIFICATION:
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o. 5635177
                                                                                                                                                            USA
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                              US/08/222,616
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                                                                                                           360 Kb floppy disk
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Pred. No. 2.5e-96;
                                                                                                                                                                                                         Blvd
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RESULT 14
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GENERAL INFORMATION:
APPLICANT: Genent
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TELEPHONE: 415/225-1994
TELEPAX: 415/952-9881
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 67.9%; Score 995; DB 1
Best Local Similarity 68.8%; Pred. No. 3e-96;
Matches 183; Conservative 37; Mismatches
                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb 1
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                         APPLICANT: Tsai, Si
APPLICANT: Wood, Wi
TITLE OF INVENTION:
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APPLICATION NUMBER: 07/826935
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
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                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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                                                                                                                 94080
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                                                                                                                                                                                                                                                                                                                                                                                                                              Application PC/TUS9504228
                                                                                                                                  USA
                                                                                                                                                                                                                                                           Tsai, Siao Ping
Wood, William I.
VENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                     Bennett, Brian
Goeddel, David
                                                                                                                                                                                                                                                                                                                Lee, James M.
Matthews, William
                                                                                                                                                                                                                                                                                                                                                                                           Genentech, Inc
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APPLICATION NUMBER: FILING DATE:

PCT/US95/04228

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 08/222616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00.000
REFERENCE/DOCKET NUMBER: 821P:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/952-9881
TELEEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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Best Local Similarity 68.8%; Pred. No. 3e-96;
Matches 183; Conservative 37; Mismatches
                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08673789 Patent No. 5814479
                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                             APPLICANT: GEORGE, F.
TITLE OF INVENTION: 18
TITLE OF INVENTION: US
TITLE OF INVENTION: ME
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN 6
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                                                                                                               NEW YORK
                                                                                                                                                 345 PARK AVENUE
                                                                                              USA
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TYROSINE KINASE AND LIGAND AND THEIR
USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
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Search completed: May Job time: 4151 sec

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FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/177,811
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026:
TELECOMMUNICATION INFORMATION:
TELEPAN: (212) 758-4800
TELEPAN: (212) 758-4800
TELEPAN: 421792
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 877
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 67.5%; Score 990; DB 2; Best Local Similarity 66.2%; Pred. No. 7.2e-96; Matches 174; Conservative 44; Mismatches 41
                                                                                                      249
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                                                                                                                                                                                                                                                        190 VALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPPRMYCSTEG 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 VCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIFLVLGTCKETFNLYYMESDD 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 LLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDEHYTPIRTYQ 69
EWLVPIGKCMCKAGYEEKNGTCQ 305
                                                                                                 EWLVPIGKCSCNAGYEERGFMCQ 271
                                                                                                                                                                                            IALVSVRVYYKKCPSVVRHLAIFPDTITGADSSQLLEVSGSCVNHSVTDDPPKMHCSAEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VCKVMEQNQNNWLLTSWISNEGASRIFIELKFTLRDCNSLPGGLGTCKETFNMYYFESDD 162
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2

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 9, 2000, 21:52:05; Search time 50.71 Seconds (without alignments) 126.581 Million cell updates/sec

Title: Perfect score: Sequence: US-09-104-340-4
1466
1 MDCQLSILLLLSCSVLDSFG......VPIGKCSCNAGYEERGEMCQ 271

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters:

188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database : A_Geneseq_36:*

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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) and	tumours of human origin, and the epithelial tumour	expressed in both pre-B	Fig .	proteins in modulating		Receptor-type tyros	WPI; 93-0363/3/04.	Boyd AD, Simpson R	INST	12-DEC-1991; AU-009992	19-JUN-1992; AUU294. 21-JUN-1991: AU-006841	07-JAN-1993.	25-A.	modified_site 779	ou/ cco arre_furnurd	† †	/no binding_site 630	binding_site 628	domain 542.		modified_site 493.	modified_site 404	:	/note modified_site 391.	/note modified_site 337.	modified_site 232.	protein 840.		/no protein 21.	tide	Key Loc	Homo sanions	Lila-1; JM; epithel	eph/elk-like; kinas	Primer; expression	24-MAY-1993 (first	R31466 standard; Pr R31466:	166 .
re useful as agents in modulation of the	, eg. lymphoid tumours LK63, Lila-1 and ur HeLa. This receptor-type thymidine)	re-B cells and T cell lines and in a number of	nglish.	pre-B, B and T cell	ke kinase, useful for phosphoryla	inase reactive with		, Wicks I	CAL RES WALTER &	992.	841		/note= "Putative autophosphorylation site"		/note= "ATP binding site"	note= "ATP binding site"	/note= "ATP binding site" 630		/note= "Transmembrane domain"		.495	/notes "N-link alvaneviation"	/note= "N-link glycosylation"		.339	.234	.860	/note= "Purified HEK protein #1"	/note= "Signal peptide" 2139		Location/Qualifiers	itat tesponse, growch, differentiation.	ype; thymidine kinas	lymphoid: LK6	in; human;	entry)	Protein; 983 AA.	

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RESULT R7571LT DE R7571LT R7571LT R7571LT R75751LT R75751
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Matches
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Best Local Similarity
Matches 240; Conser
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Gallus sp.
WO9515375-A.
08-JUN-1995.
07-SEP-1994; U10140.
03-DEC-1993; U5-162809.
(LJOL-) LA JOLLA CANCER RES FOR PASQUALE EB, Sajjadi FG;
WPI, 95-215256/28.
                                                                                                                                                                                                                                                                                                                             Disclosure; Page 85-89; 129pp; English.

Probes derived from the EPH-related PTKs Cek4 (Q90659) and Ce (Q90660) were used to isolate novel cDNA clones (Q90652-58, Q90661-62) from chicken embryo and embryonic brain libraries. Cek4 is highly expressed in the chicken developing brain and embryonic tissues and also in the adult brain and retina. Sequence 983 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              production and/or function analogues have activity in cellular responses such as Sequence 983 AA;
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R75711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eph-related protein tyrosine kinase(s) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; Q90659
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Eph-related PTK Cek4
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                                                         LAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCVNNSKEEDPP
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06-JUN-1995; 469537.

17-MAR-1995; US-406247.

26-JUL-1991; US-736559.

28-OCT-1993; US-144992.

06-JUN-1995; US-469337.
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Rat receptor tyrosine kinase Ehk-2.
Receptor tyrosine kinase; Ror-1; Ror-2; Ehk-1; Ehk-2; detection;
neurotrophin activity; trkB; proto-oncogene; tyrosine kinase receptor;
binding protein; BDNF; NT-3; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes nucleic acid molecules for ror-1 ror-2, ehk-1 and ehk-2. Also described are the corresponding pro Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor tyrosine kinases. The present sequence represents rat Ehk-2. Sequence 948 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (REGE-) REGENERON PHARM INC. Maisonplarie PC, Masiakowski WPI; 99-044584/04. N-PSDB; V70208.
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US5843749-A.
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65.7%;
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Pred. No. 4.6e-95;
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R85936 stand R85936; 14-FEB-1996

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Protein tyrosine-kinase

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Best Loca
Matches
                        Homo sapiens.
W09528484-A1.
26-OCT-1995.
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Agonist antibodies which activate specific protein tyrosine Agonist antibodies which activate proteins of kinase extracellular kinase(s) - also activate chimeric proteins of kinase extracellular domain and Ig constant domain, useful for studying, and therapeutic modulation of, cell growth and differentiation modulation of, cell growth and differentiation Disclosure; Page 95-99; 125pp; English PTK, sequences were used to screen cDNA libraries to identify novel pTK genes. The bpTKs, DpTK1, bpTK2, bpTK3, bpTK4, bpTK5 and bpTK7 (R85924-28 and R85935, respectively) are expressed in human brain tissue and show homology to known pTKs. A full-length sequence for bpTK7 (R85936) was also obtd. bpTK7 can be used to design drugs that modulate pTK activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   obtd. by
Sequence
                                                          16-APR-1996 (first entry)
EPH-like receptor protein tyrosine kinase HEK8.
EPH-like receptor protein tyrosine kinase; PTK; HEKB;
human eph-like kinase; therapy; diagnosis; vector; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-APR-1994; US-222616.
(GETH ) GENENTECH INC.
Bennett BD, Goeddel D,
                                                                                                            R85091 standard; Protein; R85091;
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                                                                                                                                                                                                                                                                                                                                                 TYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYME
                                                                                                                                                                                                                                                                                                                                                                                                LLSC--SVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYP-SHGWEEISGVDEHYTPIR
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                                                                                                                                                                                                            TEGEWLVPIGKCSCNAGYEERGFMCQ
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U04681.
US-229509.
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571. .98
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548. .57
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/label=
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Pred. No. 3.3e
37; Mismatches
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Mus sp.

US5814479-A.
29-SEP-1998.
11-JUN-1996; 673789.
04-JAN-1994; US-177812.
11-JUN-1996; US-673789.
(KROM/) KROMER L F.
(SCHULZ N T.
(WOUD/) WOUDE G F V.
(ZHOU/) ZHOU R.
KTOMER L F.
KTOMER L F.
(SCHULZ N T.
(WOUD/) WOUDE G F V.
(ZHOU/) ZHOU R.
KTOMER L F.
KTOMER SCHULZ NT, WO
WPI; 98-541751/46.
                                                                                                                                                                             Wilder, Wilder, 25-NOV-1998 (first entry)
25-NOV-1998 (first entry)
Mouse Bsk receptor-like tyrosine kinase, brain; diagnosis; neoplasm neurodegenerative disease; limbic system neuron regeneration; chromosomal abnormality, degenerative growth; development disorder; chromosomal abnormality, degenerative growth; development disorder; chromosomal abnormality, all pheimer's disease; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7, HEK8 and HEK11 (R85089-92), respectively, were identified following isolation of their encoding cDNAs (T02946-49) from a human foetal braccon library. :HEK5, HEK7 and HEK8 show extensive homology to the catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8. HEK11 shows no homology to any known EPH-like receptor. Recombinant HEK receptors (or their soluble extracellular domains) are produced to expression of encoding sequences in procaryotic or eucaryotic host cells, and are used to produce antibodies (utilised in diagnostic assays), or to identify and purify ligands for HEK receptors, or therepeutically to modulate the activation of cell-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding EPH-like receptor tyrosine kinase(s) and related vectors, host cells, proteins, antibodies etc., us diagnostically and therapeutically to modulate receptor activa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 18; Page 62-65; 133pp;
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Pred. No. 3.3e-94;
7; Mismatches 42
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PS Claim 1; Fig 2; 72pp; English.

CC The present sequence represents mouse Bsk, which is a receptor-like CC The present sequence represents mouse Bsk which is a receptor-like CC tyrosine kinase. The nucleic acid sequence encoding Bsk can be used in CC Bsk nucleic acid probes, which can be used in detecting alterations in CC the level of Bsk messenger-RNA (mRNA) in biological samples isolated CC from a mammal afflicted with a disease, such as neurodegenerative CC diseases or disorders and neoplasms. The nucleic acid sequence can also CC be delivered into the limbic system of patients with limbic system CC neurodegenerative disease, disorder or injury, to promote or enhance CC neurodegenerative disease, disorder or injury, to promote or enhance CC diseases include, chromosomal abnormalities, degenerative growth and CC development disorders, viral infections, bacterial infections, brain CC injuries, neoplastic conditions, Alzheimer's disease, epilepsy, SQ Sequence 877 AA;
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Matches
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01-DEC-1998.
06-JUN-1995; 469537.
17-MAR-1995; US-406247.
26-JUL-1991; US-73559.
28-OCT-1993; US-144992.
06-JUN-1995; US-469537.
                                                                                                                                                                                                                                                                                                    Rat receptor tyrosine kinase Ehk-1.

Receptor tyrosine kinase; Ror-1; Ror-2; Ehk-1; Ehk-2; detection; neurotrophin activity; trkB; proto-oncogene; tyrosine kinase receptoring protein; BDNF; NT-3; diagnosis.
Example; Fig 22; 194pp; English.

The present invention describes nucleic acid molecules for represent invention describes are the corresponding ror-2, ehk-1 and ehk-2. Also described are the corresponding Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan recept
                                                                                                      (REGE-) REGENERON PHARM INC.
MAISONDIETE PC, MASIAKOWSKI P, YANCOPOULOS
WPI; 99-044584/04.
N-PSDB; V70207.
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bes, used in detecting alterations in level o
biological samples isolated from mammal affl
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66.2%;
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pred. No. 9e-94;
44; Mismatches 4
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  Query Match
Best Local Similarity
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH) GENENTECH I
Caras IW, Winslow
WPI; 96-239448/24.
N-PSDB; T18893.
                                                                                                                                                treatment and diagnosis of neuronal disorders and angiogenesis-related conditions.

Example 1: Page 50-53; 75pp: English.

Rat REK7 (R97853) is an eph-related tyrosine kinase receptor, for which AL-1 (see also W97854) is a ligand. Its amino acid sequence was deduced from a cDNA clone (R18893) isolated from a hippocampal cDNA library. An REK-IGG fusion was used to screen cultured cell lines for surface expression of REK7-binding activity. Primers (see also T44382-83) based on peptide sequences (R97856-59) of isolated ligands were used to amplify human breast carcinoma BT20 cell cDNA, and an amplified fragment was used to screen a human foetal brain cDNA library, leading to the isolation of AL-1 cDNA related:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-OCT-1995; U14016.
27-OCT-1994; US-330128.
07-JUN-1995; US-486449.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-JAN 1997 (first entry)
Rat REK7 eph-related tyrosine kinase receptor.
REK7; eph-related tyrosine kinase receptor; AL-1; ligand;
neurotrophic factor; neuropathy; angiogenesis; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tyrosine kinases. The present sequence represents rat Ehk-1. Sequence 1005 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL-1 neurotrophic factor,
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                                                                                                          A
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58. .462
/label= Extracellul
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Pred. No. 1.8e
44; Mismatches
987;
No.
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No. 1.8e-93;
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Score Pred.

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Length

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                                                                                                                                                                                                                                                                               4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7, CHEK8 and HEK11 (R85089-92), respectively, were identified following isolation of their encoding cDNAs (T02946-49) from a human foetal brain CDNA library. HEK5, HEK7 and HEK8 show extensive homology to the catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8. HEK11 shows no homology to any known EPH-like receptor. Recombinant HEK receptors (or their soluble extracellular domains) are produced by expression of encoding sequences in procaryotic or eucaryotic host cells, and are used to produce antibodies (utilised in diagnostic assays), or to identify and purify ligands for HEK receptors, or therapeutically to modulate the activation of cell-associated proliferation and/or differentiation of brain cells.
                                                                                                                                                              Query Match
Best Local S
Matches 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid encoding EPH-like receptor tyrosine kinase(s) and related vectors, host cells, proteins, antibodies etc., usualisationstically and therapeutically to modulate receptor activations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-APR-1996 (first entry)
EPH-11ke receptor protein tyrosine kinase HEK7.
EPH-11ke receptor protein tyrosine kinase; PTK;
human eph-11ke kinase; therapy; diagnosis; vect
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Claim 18; Page 54-57; 133pp; English.
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N-PSDB; T02947.
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26-OCT-1995.
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Fox GM, Jing S, Welcher
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15-APR-1994; US-229509.
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                                                                          VCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDD
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VCKVMEQNQNNWLLTSWISNEGASRIFIELKFTLRDCNSLPGGLGTCKETFNMYYFESDD
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                                                                                                                                                            al Similarity 65.8
173; Conservative
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                                                                                                                                                          Score 984; DB 1;
Pred. No. 4.5e-93;
4; Mismatches 42
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or prodn.

Claim 18; Page 71-75; 133pp; English.

CL 4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7,

CC 4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7,

CC 4 Novel human EPH-like receptors protein tyrosine kinases, HEK7,

CC HEK8 and HEK11 (R85089-92), respectively, were identified following

CC isolation of their encoding cDNAs (T02946-49) from a human foetal brain

CC CDNA library. HEK5, HEK7 and HEK8 show extensive homology to the

CC catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8.

CC HEK11 shows no homology to any known EPH-like receptor. Recombinant

CC HEK receptors (or their soluble extracellular domains) are produced by

CC expression of encoding sequences in procaryotic or encaryotic host

CC cells, and are used to produce antibodies (utilised in diagnostic

CC assays), or to identify and purify ligands for HEK receptors, or

CC therapeutically to modulate the activation of cell-associated
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Sin
Matches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding EPH-like receptor tyrosine kinase(s) and related vectors, host cells, proteins, antibodies etc., used diagnostically and therapeutically to modulate receptor activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPH-like receptor protein tyrosine kinase HEK11.
EPH-like receptor protein tyrosine kinase; PTK; HEK11;
human eph-like kinase; therapy; diagnosis; antibody; vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptors.
Sequence
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Fox GM, Jing S, Welcher
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26-OCT-1995.
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                                                                                                    145
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L5-APR-1994; US-229509.
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                                                                        TIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPF 204
                                                                                                                                                                                                                                                                               QPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRT 84
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TVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKE--EDPPRMYCSTEGEWLVPIGKCSCNA
                                                 TIAADESFTQGDLGERKMKLNTEVREIGPLSKKGFYLAFQDVGACIALVSVKVYYKKCWS
                                                                                                                                                                            NWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDDDHGVKFREHQFTKID 144
                                                                                                                                                                                                                                                     QAAKEVLLLDSKAQQTELEWISSPPNGWEEISGLDENYTPIRTYQVCQVMEPNQNNWLRT 87
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                                                                                                                                                   NWISKGNAQRIFVELKFTLRDCNSLPGVLGTCKETFNLYYYETDYDTGRNIRENLYVKID
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Pred. No. 3.2e
39; Mismatches
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.2e-87;
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I IENLAIFPDTVTGSEFSSLVEVRGTCVSSAEEEAENAPRMHCSAEGEWLVPIGKCICKA

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262 GYEERGFMCQ

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268

GYQQKGDTCE

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Best Local Sim
Matches 172;
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CDNA cloning using adult mouse brains and Northern blotting identified 2 truncated versions, MDK1 T1 (W03422) and MDK1 T2 (W03423), of the novel mouse developmental kinase 1 (MDK1) (see als W03423), a new member of the eck/eph family of receptor tyrosine kinases. Their amino acid sequences were deduced from cDNA clones (T32961 and T32962) obtd. from adult mouse brains. MDK T1 and T2 each possess the entire ectodomain, the transmembrane domain and part of the juxtamembrane region of MDK1, but lack the catalytic tyrosine kinase domain. They can be used to screen for potential agents useful for treatment of diseases characterised by abnormal signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SUGE-) SUGEN INC.
Ciossek T, Millau
WPI: 96-333988/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JUL-1996.
03-JAN-1996; U00419.
03-JAN-1995; US-368776.
(PLAC) MAX PLANCK GES
                                                                                                                                                                                                                                                                                                                                                                                                                                                         New mouse development kinase 1 gene - use diagnosis and treatment of abnormalities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified_site
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Mouse developmental kinase 1; MDK1 T1; receptor tyrosine kinase; RTK; signal transduction; probe; diagnosis; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                               pathways
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  208
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            TVKNLAMEPDTVP-MDSQSLVEVRGSCVNNSKE--EDPPRMYCSTEGEWLVPIGKCSCNA
                                                               TIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPF
                                                                                                   NWISKGNAQRIFVELKETLRDCNSLPGVLGTCKETFNLYYYETDYDTGRNIRENLYYKID
                                                                                                                  NWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDDDHGVKFREHQFTKID
                                                                                                                                                       QAAKEVLLLDSKAQQTELEWISSPPSGWEEISGLDENYTPIRTYQVCQVMEPNQNNWLRT
                                                                                                                                                                    QPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRT
IVENLAVFPDTVTGSEFSSLVEVRGTCVSSAEEEAENSPRMHCSAEGEWLVPIGKCICKA
                                                 TIAADESFTQGDLGERKMKLNTEVREIGPLSKKGFYLAFQDVGACIALVSVKVYYKKCWT
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600. .61
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/label=
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64. .66
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                                                                                                                                                                                                                      63.2%;
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                                                                                                                                                                                                          Score 926.5;
Pred. No. 1.9e
37; Mismatches
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les in signal transduction
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Best Local S
Matches 172
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03-JAN-1996; U0-388776.
03-JAN-1995; US-388776.
(PLAC ) MAX PLANCK GES FC
(SUGE-) SUGEN INC.
Clossek T. Millauer B,
                                                                                                                                                                                                                                                                    Example 1; Page 113-115; 128pp; English.

Example 1; Page 113-115; 128pp; English.

CDNA cloning using adult mouse brains and Northern blotting identified 2 truncated versions, MDKI TI (W03422) and MDKI T2 (W03422), of the novel mouse developmental kinase 1 (MDKI) (see als W03421), a new member of the eck/eph family of receptor tyrosine kinases. Their amino acid sequences were deduced from cDNA clones (T32961) and T32962) obtd. from adult mouse brains. MDK TI and T2 each possess the entire ectodomain, the transmembrane domain and part of the juxtamembrane region of MDKI, but lack the catalytic tyrosine kinase domain. They can be used to screen for potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse developmental kinase 1 MDK1 T2.
Mouse developmental kinase 1; MDK1 T2; receptor tyrosine kinase;
RTK; signal transduction; probe; diagnosis; gene therapy;
neurodegeneration; neuroproliferation; cancer.
                                                                                                                                                                                                                                                     agents useful for treatment of diseases characterised by abnormal signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 96-333988/33.
N-PSDB; T32962.
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             205
                                     148
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                                                                                                                                                                               Local Similarity 68.8 hes 172; Conservative
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                                 GYQQKGDTCE
             TVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKE--
                                                                                                                               QAAKEVLLLDSKAQQTELEWISSPPSGWEEISGLDENYTPIRTYQVCQVMEPNQNNWLRT 87
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                                                                                                                                                                                                                                          626 AA;
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555. .57
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343. .34
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                                                                                                                                                                              37;
                                                                                                                                                                             Score 926.5; |
Pred. No. 2e-8
37; Mismatches
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            EDPPRMYCSTEGEWLVPIGKCSCNA
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n signal transduction
DB 1;
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Best Local S
Matches 172
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20 Mouse developmental kinase 1 (MDK1) (W03421) is a new member of the ceck/eph family of receptor tyrosine kinases (RTKS). Its amino acid sequence was deduced from a cDNA clone (T32960) isolated from mouse embryo and adult brain libraries. The distinct patterns of MDK1 expression during mouse development suggest an important role for MDK1 in the formation of neuronal structures.

21 MDK1 may be obtd. by expression in host cells. It can be used in methods for the diagnosis of diseases characterised by abnormality in a signal transduction pathway, such as neuroproliferative or neurodegenerative disorders or cancer, to screen for (ant)agonists, and to raise antibodies.
                                                                                                                                                                                                                                                                                                                diagnosis and treatment pathways
                                                                                                                                                                                                                                                                                                                                                    (PLAC) MAX PLANCK GES (SUGE-) SUGEN INC.
Clossek T, Millauer B, WPI; 96-333988/33.
                                                                                                                                                                                                                                                                                                                                                                                        11-JUL-1996.
03-JAN-1996; U00419.
03-JAN-1995; US-368776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse developmental kinase 1.

Mouse developmental kinase 1; MDK1; receptor tyrosine signal transduction; probe; diagnosis; therapy; neurodegeneration; neuroproliferation; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                         New mouse development kinase 1 gene - use diagnosis and treatment of abnormalities
                                                                                                                                                                                                                                                                                                                                             N-PSDB; T32960
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                                                                                                   TVKNLAMEPDTVP-MDSQSLVEVRGSCVNNSKE--EDPPRMYCSTEGEWLVPIGKCSCNA
                                       TIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPF
                                                                NWISKGNAQRIFVELKFTLRDCNSLPGVLGTCKETFNLYYYETDYDTGRNIRENLYVKID
                                                                           NWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDDDHGVKFREHQFTKID
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                             TIAADESFTQGDLGERKMKLNTEVREIGPLSKKGFYLAFQDVGACIALVSVKVYYKKCWT
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                                                                                                                                                    Score 926.5; DB Pred. No. 4e-87;
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AC R7
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R75712;
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(LJOL-) LA J
Pasquale EB,
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Query Match
Best Local Sim
Matches 139;
Cek5+; Eph; protein tyros
prognosis.
Gallus sp.
W09515375-A.
08-JUN-1995.
07-SEP-1994; U10140.
03-DEC-1993; US-162809.
(LJOL-) LA JOLLA CANCER R
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Gallus sp.
WO9515375-A.
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07-SEP-1994;
03-DEC-1993;
                                                                                                              Eph-related PTK
Cek5+; Eph; prot
                                                                                                                                                           R75709 standard; R75709;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Probes derived from the EPH-related PTKs Cek4 (Q90659) and Cek5 (Q90660) were used to isolate novel cDNA clones (Q90652-58, Q90661-62) from chicken embryo and embryonic brain libraries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pasquale EB, Sajj
WPI; 95-215256/28.
                                                                                                                                             11-NOV-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 92-96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eph-related protein tyrosine kinase(s) -
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(LJOL-) LA JOLLA CANCER
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995 AA;
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                                                                                                            tyrosine-kinase;
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55.4%;
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Pred. No. 3.8e
51; Mismatches
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.8e-71;
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                                                                                                                                                                                                                                                                                                                                WPI; 95-215256/28.

N-PSDB; Q90657.

Eph-related protein tyrosine kinase(s) - for monitoring and diagnosing cancer.

Claim 11; Page 71-75; 129pp; English.

A cDNA clone encoding a novel variant of EPH-related PTK Cek5,

Cek5+ (Q90657), was isolated from a chick embryo library in lambda gtll. Cek5+ protein (R75709) contains a 16-amino acid insertion in the juxtamembrane domain, and be a result of alternative splicing. Cek5+ is exclusively expressed in the CNS. Sequence 1011 AA;
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                                                      YESVENGTVCR 278
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Title:
Perfect score:
Sequence:
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O4356 homo sapten
O95143 homo sapten
O95142 homo sapten
O95142 homo sapten
O97173 xenopus lae
O07498 gailus gall
O60659 mus musculu
O91736 xenopus lae
O07494 gailus gall
O73878 brachydanio
O08644 mus musculu
O15197 homo sapten
O9xz16 drosophila
O9xz16 drosophila
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Q91845 xenopus lae
Q91845 xenopus lae
Q91842 gallus gall
Q73879 brachydanio
Q13146 brachydanio
Q43477 homo sapien
Q91571 xenopus lae
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Batrachia;
                                                                                                                                                                                                                    -I- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY (BY SIMILARITY). MAY PLAY A ROLE IN THE DIFFERENTIATION OF CRANIAL NEURAL CREST AND OTHER TISSUES.
-I- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.
-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-I- TISSUE SPECIFICITY: LOCALIZED EXPRESSION IN A SUBSET OF NEURAL CREST AND NEURAL TISSUES IN EMBRYOS.
-I- DEVELOPMENTAL STAGE: PRESENT TRANSIENTLY IN VISCERAL ARCH 3. ALSO EXPRESSED IN THE FOREBRAIN, RHOMBOMERES R3 AND R5 OF THE HINDBRAIN AND IN THE PRONEPHROS.
-I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
-I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-I- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN BEYONGS TO THE FEBRUARY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Xenopus.
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Q91694;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
TYROSINE-PROTEIN KINASE RECEPTOR PAG PRECURSOR (E)
   DOMAIN. BELONGS TO THE EPH FAMILY.
EMBL; L26099; AAA64464.1; -.
HSSP; P00523; 2PTK.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS00109; PROTEIN_KINASE_TYR;
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WINNING R.S., SARGENT T.D.;

"Pagilaccio, a member of the Eph family of receptor tyrosine kinase genes, has localized expression in a subset of neural crest and neur tissues in Xenopus laevis embryos.";

Mech. Dev. 46:219-229(1994).
                                                                                                                                                                                                                                    <del>+</del> <del>+</del> <del>+</del> <del>+</del>
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TISSUE=NEURAL CREST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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PAG.
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PROTEIN_KINASE_ATP; 1.
PROTEIN_KINASE_TYR; 1.
RECEPTOR_TYR_KIN_V_1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              precursor (EC 2.7.1.112)
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Best Local S
Matches 159
SEQUENCE FROM N.A.

MEDLINE; 96125143.

XU Q., ALLDUS G., HOLDER N., WILK
"Expression of truncated Sek-1 re
"Expression extriction of gene exp
hindbrain.";

Development 121:4005-4016(1995).

-:- FUNCTION: RECEPTOR FOR MEMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE: PS00791; RECEPTOR PRAM; PF00041; fn3; 2.
PEAM; PF000069; pkinase; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF01404; EPH_lbd; 1.
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                                                                                                                                                                                                      Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                                             SEK-1.
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(TIEMBLrel. 01, Last sequence update)
(TIEMBLRel. 12, Last annotation update)
DTEIN KINASE RECEPTOR SEK-1 PRECURSOR (EC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74.5%;
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                                                              N., WILKINSON D.
Sek-1 receptor t
gene expression
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TYROSINE-PROTEIN KINASE RECEPTOR PIEXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE DOMAIN (BY SIMILARITY FIBRONECTIN TYPE-III (BY SIMILARITY FIBRONECTIN TYPE-III (BY SIMILARITY PROTEIN KINASE.
      MEMBERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
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BY S
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; 026BA8A5 CRC32;
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                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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No. 1.8e-79;
        မှု
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      THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal; Repeat;
                                                                tyrosine x
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      EPHRIN-A
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                                                                e kinase
Xenopus
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        FAMILY
                                                                                                                                                                                                           Amphibia;
Xenopodinae;
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                                                                                                                                                                                                                                                                                              2.7.1.112).
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SIMILARITY).
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                                                                disrupts the and zebrafish
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042422;
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Query Match
Best Local S
Matches 159
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EMBL; X91191; CAA65601.1; -.

HSSP; P00523; 2PTK.

HSSP; P00523; PTK.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROM; PF00041; fn3; 2.

PFAM; PF00069; Pkinase; 1.

PFAM; PF001404; EPH_Lbd; 1.

PFAM; PF001404; EPH_Lbd; 1.

PFAM; PF001019; TYRKINASE.

PRINTS; PR001014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
CHAIN
DOMAIN
DOM
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Receptor; Tr
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AT LOWER LEVELS IN R2.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY). REQUIRED FOR INTERACTIONS IDENTITY OR MOVEMENT OF CELLS.
CATALYTIC ACTIVITY: AIP + A PROTEIN TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE F
                                                                                                                                                                                                                                                                                                                                                                                              WEEVSIMDEKNIPIRTYQVCNVMESSQNNWLRTDWIPRSGAQRVYVEIKFTLRDCNSLPG
                                                                                                                                                                                                                                                                                                                                                                                                                      WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL
                                                                                                                                                                                                                              GPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSC
                                                                                                                                                                                                                                                                                                                            VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV
                                                                                                               VDNSEEKDVPKMYCGADGEWLVPIGNCLCNAGFEEHNGGCQ
                                                                                                                                                          VNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
                                                                                                                                                                                                           GPLSKKGFYLAFQDVGACIALVSVRVFYKKCPLTVRNLAQFPDTITGSDTSSLVEVRGSC
                                                                                                                                                                                                                                                                                                    VMGTCKETFNLYYYESNNDKERFIRETQYVKIDTIAADESFTQVDIGDRIMKLNTEVRDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 71.9
39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     se; Tyrosine-protein
Transmembrane; Glycc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           986
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1 15
1 986
6 547
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325
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1745
7745
778
3407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 894.5; 1
Pred. No. 1.9e
33; Mismatches
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ATP (BY SIMILARITY).
BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
CYTOPLASMIC (POTENTIAL)
IG-LIKE C2-TYPE DOMAIN
CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
TYROSINE-PROTEIN KINASE R
EXTRACELLULAR (POTENTIAL)
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FIBRONECTIN TYPE-III
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         028DBBDA CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             894.5;
No. 1.
  993
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; Signal; Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ..9e-79;
nes 28;
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S IN R3,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13;
                                                                                                                                                             220
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THE CATALYTIC
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SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        986;
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(TrEMBLrel.

95,

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Query Match
Best Local Similarity
Matches 155; Conser
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DISULFID
BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
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DOMAIN
DOMAIN
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DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARAUJO M., NIETO M.A.;
"The expression of chick EphA7 during segmentatio peripheral nervous system.";
Mech. Dev. 68:173-177(1997).
-1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM; PF00041; fn3; 2.
PFAM; PF00069; pkinase; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF01404; EPH_lbd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNĀL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00109; TYRKINASE. PRINTS; PR00014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1;
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATAI DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY. TYPE DOMAIN.
-i- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
-i- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1999 (TIEMBLIEL. 12, Last annotation update)
EPH-LIKE RECEPTOR TYROSINE KINASE PRECURSOR (EC 2.7.1.112) (TYROSINE-
PROTEIN KINASE RECEPTOR CEPHA7).
                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE; 98092111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
       61
                                         55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYROSINE PHOSPHATE.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: WITHIN THE NERVOUS SYSTEM, EXPRESSION IS TISSUE SPECIFICITY: WITHIN THE NERVOUS SYSTEM, EXPRESSION IS RESTRICTED TO PROSOMERES I AND 2 IN THE DIENCEPHALON AND ALL THE RHOMBOMERES IN THE HINDBRAIN DURING SEGMENTATION STAGES. LATER ON, A SUPERLINGSED PATTERN APPEARS THAT CORRELATES WITH THE FORMATION OF SEVERAL AXONAL TRACTS. IN THE SOMITIC MESODERM, THE EXPRESSION OF SEVERAL AXONAL TRACTS. IN THE GUIDANCE OF BOTH NEURAL CREST AND MOTOR AXONS THROUGH THE SCLEROTOMES.
                                 VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y14271; CAA74643.1;
P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane; Glycoprotein; Signal; Immunoglo
1 30 POTENTIAL.
31 993 EPH-LIKE RECEPTOR TYROSINE
31 551 EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                           31
552
573
67
                                                                                                                  Conservative
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551
551
572
993
116
328
889
536
642
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753
786
343
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                                                                                                                               71.9%;
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                                                                                                                39;
                                                                                                              Score 862.5;
Pred. No. 2.6e
39; Mismatches
                                                                                                                                                                                                                                                                                   PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY.
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.

CYTOPLASMIC (POTENTIAL).

CYTER C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                PHOSPHORYLATION (AUTO-) (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                              FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                                                                                                                                                     IG-LIKE C2-TYPE
CYS-RICH.
                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                during segmentation
                                                                                                                                                                                                            6B6BFD17 CRC32;
                                                                                                              5; DB 13;
2.6e-76;
nes 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                ХВ)
ХВ)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IN THE CATALYTIC
                                                                                                                Indels
                                                                                                                                                 Length
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                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KINASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  central
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                                                                                                            Gaps
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013146 013146;

PRELIMINARY;

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RESULT
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AC 01
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073879
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                                                                                                                                                                       δÃ
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Best Local Similarity
Matches 149; Conser
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073879;
01-AUG-1998
01-AUG-1998
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COOKE J.E. Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1998 (TIEMBLIEL. 07, Created)
01-AUG-1998 (TIEMBLIEL. 07, Last sequence update)
01-NOY-1999 (TIEMBLIEL. 12, Last annotation update)
EPH-LIKE RECEPTOR TYROSINE KINASE RTK4 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COOKE J.E., XU Q., WILSON S
Dev. Genes Evol. 206:515-53
EMBL; AJ005030; CAA06303.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neopterygii; Teleostei; I
Cyprinoidea; Cyprinidae;
[]]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2;
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00107; PROTEIN_KINASE_APP; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. COOKE J.E., XU Q.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. COOKE J.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brachydanio rerio (Zebrafish)
Eukaryota; Metazoa; Chordata;
                                                                                                                                181
                                                                                                                                                                           182
                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
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                                                                                                                             HSEEQEVPKMYCGADGEWLVPIGNCLCNPGYEERNEQCQ
                                                                                                                                                                         NSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
                                                                                                                                                                                                           SRAGEYLAFQDVGACIALVSVHVFYKKCPLAVRNLAQEPDTVTGADTSSLVEVRGSCVD
                                                                                                                                                                                                                                         VNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCVN
                                                                                                                                                                                                                                                                                                                                  GTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGP 122
                                                                                                                                                                                                                                                                                                                                                                                           EVSIMDEKNIPIRTYQVCNVMEPSQNNWLRTHWIQRGAAQRIYIEIKFTLRDCNSLPGVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VNNSKE--EDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTCKETFNLYYLESDSDNERYAHESRFSKIDTVAADESFTQVDIGDRIMKLNTEVRDVGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSSAEEEAENSPKMHCSAEGEWLVPIGKCICKAGYQQKGDTCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPLSKKGFYLAFQDVGACIALVSVKVYYKKCWSIIENLAIFPDTVTGSEFSSLVEVRGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF001404; EPH_lbd;
PF00069; pkinase;
PF00041; fn3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZDB-GENE-990415-61; rtk4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MAR-1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       880
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98862 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ដូ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   afish) (Zebra danio).
rdata; Craniata; Vertebrata;
Euteleostei; Ostariophysi;
; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N S.W., HOLI
-531(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 838.5; DB Pred. No. 5e-74; 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7C139606 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOLDER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13;
                                                                                                                                219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 880;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                  180
                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                         120
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                                                                                                                                                                                                                                                                                                                                                                                                                                       62
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δÃ
                                Query Match
Best Local Similarity
Matches 137; Conserv
                                                                                                                                                                                                                                                                                                                                                       EMBL; U89295; AAC60220.1; -.
HSSP; P00523; 2PTK.
ZFIN; ZDB-GENE-990415-58; zekl.
ZFIN; ZDB-GENE-990415-58; zekl.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; FA
PFAM; PF000641; EPH_1bd; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF00641; EPH_1bd; 1.
                                                                                   NP_BIND
DISULFID
BINDING
BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1997
01-JUL-1997
01-NOV-1999
EPH-LIKE KINJ
RECEPTOR ZEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; C
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                  DOMAIN
DOMAIN
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DOMAIN
DOMAIN
                                                                                                                                                                                                                                                     TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                          CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BOVENKAMP D.E., GREER P.;
"Novel Eph-family receptor tyrosine kinase developing zebrafish nervous system.";
Dev. Dyn. 209:166-181(1997).
-I- FUNCTION: RECEPTOR FOR MEMBERS OF THE
                                                                                                                                                                                                                                                                                                                         PFAM; PF00041; fn3; 2.
PRINTS; PR00109; TYRKINASE.
PRINTS; PR00014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 97329578.
                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -
                                                                                                                                                                                                                                                                                                        Receptor;
                                                                                                                                                                                                                                                                                                                Transferase; Tyrosine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
L; U89295; AAC60220.1; -.
P; P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: TYPE
TISSUE SPECIFICITY: WIDELY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYSTEM.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NERVOUS SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ROLE IN EARLY PATTERN FORMATION
WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKETLRDCNSIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KINASE
2EK1).
                                                                                                                                                                                                                                                                                                        Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TremBLrel. 04, Created)
(TremBLrel. 04, Last sequence update)
(TremBLrel. 12, Last annotation update)
NASE 1 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE
                                                                                                       Conservative
                                                                                                        63.0%;
                                                                                    109654
                                                                                                                                                                                                                                                                                Glycoprotein; Signal;
BY SIMILARITY.
EPH-LIKE KINASE 1.
                                ; Score 755.5; DB
; Pred. No. 8e-66;
37; Mismatches 4
                                                                                     ₹
                                                                                        ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
S -> N.
                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
CYS-RICH.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                              PROTEIN
ATP (BY
BY SIMIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXPRESSED I
                                                                                   -> N.
10D38182
                                                                                                                                                                              SIMILARITY.
                                                                                                                                                                                      (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kinase is widely .";
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                                                                                                                                                                                                                                                                                                      Signal;
                                                                                                                                                                                                                                                                                                                                                                                       1.
FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ä
                                                                                    CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN.
IN THE DEVELOPING ZEBRAFISH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPHRIN-B FAMILY.
                                46;
                                                                                                                                                                                                                                                                                                       Immunoglobulin
                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ДĄ
                                                                                                                                                                                                                                                                                                               Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cypriniformes;
                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Actinopterygii;
                                                                                                                                               (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               + PROTEIN
                                                                                                                                               SIMILARITY)
                                                     981;
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                                                                                                                                                                                                                                                                                                        domain
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                               Gaps
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                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P00523; 2PTK.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PFAM; PF001404; EPH_1bd; 1.

PFAM; PF00041; ffn3; 2.

PFAM; PF000536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            043477;
01-JUN-1998
01-JUN-1998
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TANG X.X., PLEASURE D.E., Submitted (SEP-1997) to t EMBL; AF025304; AAB94602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE; 96.54673.

IKEGAKI N., TANG X.X., LIU X.G., BIEGEL J.A.,

SULMAN E.P., BRODEUR G.M., PLEASURE D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0014; FNTYPEIII.
PRINTS; PRO0109; TYRKINASE.
Tyrosine-protein kinase.
SEQUENCE 1055 AA; 117492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. TANG X.X., PLEASUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       043477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN-TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EPHT3):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecular characterization and chrone EPHT3): a developmentally regulated ene of the EPH family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      172
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                                                                                                                                    103
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                                                                                                                                                                                                                                                                                                            Local Similarity
mes 127; Conser
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                                                                                                                                                                                                                                               1 WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mol.
                                                                                                                               WEEVSGYDENMNTIRTYQVCNVFESSQNNWLRTKFIRRRGAHRIHVEMKFSVRDCSSIPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCVEDAEELEGPRMFCSADGGWLVPIGRCVCRPGFEEVDGHCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCYNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPGTCKETFNVYYHESNNAVAAPLRHIRESQYIKIDTIAADESFTQTDVGDRVMKLNTEV
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                                                                        IREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RDISGLSKRGLYLAFQDLGACIALVSVRVFYKRCPLAVLNLARFPDTVTGGDSALVEVRG
                                             VRSFGPVSRSGFYLAFQDYGGCMSLIAVRVFYRKCPRIIQNGAIFQETLSGAESTSLVAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genet.
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                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Catarrhini;
                                                                                                                                                                                                                                                                                                                                     559
                                                                                                                                                                                                                                                                                                                                                                                                                       117492
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. 06, Last sequence upo
. 12, Last annotation of EPHB2V.
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                                                                                                                                                                                                                                                                                                              49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                              Score 708;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata;
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lated human p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hominidae;
                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                 ; DB 4; Length 1055;
4e-61;
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                                                                                                                                                                                                                                                                                                            44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  databases
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kinase
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RGSCIANAEEVDVPIKLYCNGDGEWLVPIGRCMCKAGFEAVENGTVCR 270

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PROSITE: PS00343; GRAM_POS_P
PROSITE: PS00107; PROTEIN_KI
PROSITE: PS00109; PROTEIN_KI
PROSITE: PS00790; RECEPTOR_T
PROSITE: PS00791; RECEPTOR_T
PROSITE: PS00791; RECEPTOR_T
PROSITE: PS000791; FALSE
PFAM; PF00069; PK1nase; 1.
PFAM; PF00069; PK1nase; 1.
PFAM; PF00104; EPH_1bd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1996
01-NOV-1996
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Q91571;
                                          NP_BIND
DISULFID
BINDING
ACT_SITE
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- DEVELOPMENTAL STAGE: MATERNALLY EXPRESSED, IT DECREASES AT MID BLASTULA TRANSITION AND REAPPEARS AT LATE NEURULATION. EXPRESSED AT HIGHER LEVELS IN THE ANTERIOR AND DORSAL REGIONS OF EMBRYONIC STAGES 16, 24 AND 37. IN ADULT IT APPEARS TO BE UBIQUITOUSLY EXPRESSED WITH HIGHER EXPRESSION IN BRAIN AND OVARY. EXPRESSION ITHE BRAIN, BRACHIAL ARCHES, TRIGEMINAL FACIAL GANGLION, AND THE RETINA OF SWIMMING TADPOLE STAGE OF DEVELOPMENT.
-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALLYIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
EMBL: U14164; DAA74888.1; -.
                                                                                                                                                                                                                         DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                           DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                  Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JONES T.L., KARAVANOVA I., MAENO M., ONG R.C., KUNG H.-F., DAAR I.O.;
"Expression of an amphibian homolog of the Eph family of receptor
tyrosine kinases is developmentally regulated.";
Oncogene 10:1111-117(1995).
Oncogene 10:111117(1995).
Oncogene 10:11117(1995).
Oncogene 10:111117(1995).
Oncogene 10:111117(1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KINASE RECEPTOR
                                                                                                                                                       DOMAIN
                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; U14164;
; P00523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "-1996 (TIEMBLIFEL 01, Created)
"-1996 (TIEMBLIFEL 01, Last sequence update)
"-1999 (TIEMBLIFEL 12, Last annotation update)
"IPPE-B RECEPTOR XEK PRECURSOR (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95215070.
                                                                                                                                                                                                                                                                                                                                                                                                       Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                        Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; GRAM_POS_ANCHORING; UNKNOW
; PROTEIN_KINASE_ATP; 1.
; PROTEIN_KINASE_TYR; 1.
; RECEPTOR_TYR_KIN_V_1; FALS
L; RECEPTOR_TYR_KIN_V_2; 1.
Glycoprotein;
POTENTIAL.
                                                             PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY.
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL) IG-LIKE C2-TYPE DOMAIN.
                PHOSPHORYLATION (AUTO-) (POTENTIAL). POTENTIAL.
                                                                                                                                                                         FIBRONECTIN TYPE-III.
                                                                                                                                                                                                 FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                           POLY-LEU.
EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                        EPHRIN TYPE-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              985
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                                                                                                                                                                                                                                                                                                                                                                                                   Signal;
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                                                                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                           RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                     Immunoglobulin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amphibia;
Xenopodinae;
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O43569
C 043569;
O1-JUN-1998 (TrEMBLrel. 06, Created)
T 01-JUN-1998 (TrEMBLrel. 06, Last sequence updat
O1-JUN-1998 (TrEMBLrel. 12, Last annotation upd
EPH-LIKE RECEPTOR TYROSINE KINASE HEPHB1C
FPH-LIKE RECEPTOR TYROSINE KINASE HEPHB1D).
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043569
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Best Local
                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                             STEIN E., SCHÖECKLMANN H.O., SUDMITTED (DEC-1997) to the E EMBL; AF037333; AAB94627.1; -EMBL; AF037334; AAB94628.1; -EMBL; AF037334; AAB94628.1; -PSAM; PF00069; Pkinase; 2. PFAM; PF00069; Pkinase; 2. PFAM; PF00536; SAM; 1. PFAM; PF019404; EPH_Lbd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
SEQUENCE
                                                                                                                                                                                                              PRINTS;
                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                      Eutheria;
             176
                                162
                                                                       102
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                                                                   WEEISGYDEHYTPIRTYQYCNYMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VPGSCKETFNLYYYETDSNIENKISTFWNESPYLKVDTIAADESFSQVDFGGRLMKVNTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL 60
RGSCVNNSKEEDPP-RMYCSTEGEWLVPIGKCSCNAGYE-ERGFMCQ
                              VRSEGPLTRNGFYLAFQDYGACMILLSVRVFFKKCPSIVQNEAVFPETMTGAESTSLVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLGTCKETFNLYYMESDDDHGVK-----FREHQFTKIDTIAADESFTQMDLGDRILKLNTE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGSCVNNSKEEDPP-RMYCSTEGEWLVPIGKCSCNAGYE-ERGFMCQ
                                       IREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RGTCIPNAEEVDVPIKLYCNGDGEWMVPIGKCTCKAGYEPENHVVCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  al Similarity
125; Conserv
                                                                                                                                                    al Similarity
123; Conserv
                                                                                                                                                                                                              PR00109;
PR00014;
                                                                                                                                                                                                                                                                                                                                                      Primates;
                                                                                                                                                                                                                                                                                                                                                            ns (Human)
Metazoa; (
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985
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                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΑA;
                                                                                                                                                                                                 ; TYRKINASE.
; FNTYPEIII.
AA; 105291 MW;
                                                                                                                                                                                                                                                                                                                                                    Chordata; C:
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110104 MW;
                                                                                                                                                            56.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57.6%;
55.1%;
                                                                                                                                                                                                                                                                                                              H.O.,
                                                                                                                                                                                                                                                                                  .' .'
                                                                                                                                               Score 676.5; DB 4;
Pred. No. 4.3e-58;
                                                                                                                                                                                                                                                                                                   EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 691.5; DB 1
Pred. No. 1.5e-59;
                                                                                                                                                                                                                                                                                                              DANIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.

1; 2416A8F9 CRC32;
                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata;
i; Hominidae; Homo.
                                                                                                                                                                                                  C4C78A21 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                              update)
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                                                                                                                                                                                                                                                                                                   databases.
                                                                                                                                                                   Length
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                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                              Mammalia;
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                                                                                                                                                                    943;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     985;
                                                                                                                                                 7;
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                                                                                                                                                 Gaps
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                                                                                                                              60
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                                                                    161
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222

RGTCIPNAEEVDVPIKLYCNGDGEWMVPIGRCTCKPGYEPENSVACK 268

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RESULT
OPSILE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 56.4
Best Local Similarity 54.3
Matches 123; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 095143
095143;
01-MAY-1999
01-MAY-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-KIDNEY;
STEIN E. SCHOECKIMANN H.O.,
Submitted (NOV-1997) to the I
EMBL; AF037332; AAD02031.1;
HSSE; P00523; 2PTK.
                            PROSITE;
PROSITE;
                                                                          "Nck recruitment to Eph rec
to c-Jun Kinase.";
J. Biol. Chem. 0:0-0(1997).
EMBL; AF037331; AAD02030.1;
HSSP; P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          095142
                                                                                                                                                                                            TISSUE-KIDNEY;
STEIN E., HUYNH-DO U.,
                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-NOV-1999 (TrEMBLrel. 12,
EPH-LIKE RECEPTOR TYROSINE K
                                                                                                                                                                                                                                                                                                               Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
         Receptor;
                                                                                                                                                                                                                                                                                                                                                             EPHB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPH-LIKE RECEPTOR
                                                                                                                                                                                                                                                                                       Sutheria;
                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGSCVNNSKEEDPP-RMYCSTEGEWLVPIGKCSCNAGYE-ERGFMCQ 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPGSCKETFNLYYYETDSVIATKKSAFWSEAPYLKVDTIAADESFSQVDFRGRLMKVNTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VLGTCKETFNLYYMESDDDHGVK----FREHQFTKIDTIAADESFTQMDLGDRILKLNTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WEEVSGYDENLINTIRTYQVCNVFEPNQNNWLLTTFINRRGAHRIYSEMRFTVRDCSSLPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VRSFGPLTRNGFYLAFQDYGACMILLSVRVFFKKCPSIVQNFAVFPETMTGAESTSLVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IREVGPVNKKGEYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RGTCIPNAEEVDVPIKLYCNGDGEWMVPIGRCTCKPGYEPENSVACK
                     0523; 2PTK.
PS00107; PROTEIN_KINASE_ATP;
PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kinase.
973 AA
                                                                                                                                                                                                                                                                                       Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primates;
                                                                                                                                                                                                                                                                                                             Metazoa;
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ABLrel. 10,
ABLrel. 12,
TYROSINE F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108938
                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Mammalia; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                        Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56.4%;
                                                                                                                                                                                       LANE
                                                                                                                                                                    receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Last sequence up, Last annotation KINASE HEPHB1B.
                                                                                                                                                                                                                                                                                                                                                                              , Last sequence update)
, Last annotation updat
KINASE HEPHB1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45;
                                                                                                                                                                                       Α.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , DANIEL T.O.;
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                 CERRETTI D.P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ed. No. 4.5
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       548C281A CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              676.5; DB 4
No. 4.5e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             973
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                                                                                                                                                                                       .P.,
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                                                                                                                                                                    couples
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   databases
                                                                                                                                                                                       DANIEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                             Mammalia;
                                                                                                                                                                 L T.O.;
ligand
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                                                                                                                                                                    activation
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Q91735;
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Best Local S
Matches 123
                                                      EMBL; L43620; AAA93526.1; -.
HSSP; P00523; 2PTK
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PRAM; PF000401; ffn3; 2.
PFAM; PF00069; pkinase; 1.
PFAM; PF001404; EPH_Lbd; 1.
PFAM; PF001404; PEPH_Lbd; 1.
PRINTS; PR00109; TYRKINASE.
PRINTS; PR00104; PYTYPEIII.
                                                                                                                                                                                                                                                                                                              -I- CAPALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
TYROSINE PHOSPHATE.
-I- SUBCELJULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-I- TISSUE SPECIFICITY: EXPRESSED IN THE EMBRYO IN PRE-SOMITIC
MESODERM, CAUDAL SOMITES, MIDBRAIN, AND CEMENT GLAND. MOST
ABUNDANT IN ADULT BRAIN, EYE, HEART, LUNG AND OVARY. LOWER LEVELS
IN INTESTINE, KIDNEY, OVLDUCT AND PHARYNX.
-I- DEVELOPMENTAL STAGE: EXPRESSED DURING EARLY DEVELOPMENT.
-I- SIMILARITY: COTTAINS 1 INMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
-I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 96068901.
SCALES J.B., WINNING R.S., RENAUD (
"Novel members of the eph receptor during Xenopus development.";
Oncogene 11:1745-1752(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TIEMBLIE) 01, Created)
01-NOV-1996 (TIEMBLIE) 01, Last sequence update)
01-NOV-1999 (TIEMBLIE) 12, Last annotation update)
01-NOV-1999 (TIEMBLIE) 12, Last annotation update)
EPHRIN TYPE-B RECEPTOR PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                     Transferase; Tyrosine-protein kinase;
Receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KINASE RECEPTOR)
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Glycoprotein;
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Pred. No. 4.6e
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Xenopodinae;
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Best Local Similarity
Matches 122; Conserv
                                                                                    EMBL; Z19061; CAA79511.1; -.

HSSB; P00523; 2PTK.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PFAM; PF001404; EBH_lbd; 1.

PFAM; PF00041; fn3; 2.

PFAM; PF00536; SAM; 1.

PFAM; PF00536; SAM; 1.
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Eukaryota; Metazoa; Chordata;
Neognathae; Galliformes; Phasi
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996 (TrEMBLrel. 01, Last sequence update)
999 (TrEMBLrel. 12, Last annotation update)
KINASE CEK10 RECEPTOR (EC 2.7.1.112) (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
C5CA9B7B CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BD419F6D CRC32;
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No. 9.5e-57;
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SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₽
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Best Local S
Matches 117
                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                   Matches
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Q60669;
Q1-NOV-1996
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPHB3 OR ETK2.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                             PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrembLrel. 01, 01-NOV-1996 (TrembLrel. 01, 01-NOV-1999 (TrembLrel. 12, PROTEIN KINASE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U11493; AAA67925.1;
HSSP; P00523; 2PTK.
MGD; MGI:104770; Ephb3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 95200798.
                                                                                                                                                                                                                                                                                                                                              PFAM;
 117
                                     119
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                                                                                                                                                                                                                                                                                                                                         1; PF01404; EPH_1bd; 1.
1; PF00041; fn3; 2.
1; PF00536; SAM; 1.
1; PF00069; pkinase; 1.
                                                                                                                                        WEEISGVDEHYTPIRTYQVCNYMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL
SFGPLSKAGFYLGFQDQGACMSLISVRAFYKKCASTTAGFALFPETLTGAEATSLYIAPR
                  EVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRG
                                                                 GTCKETFNLYYMESDDD----HGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIR | :||||||| | :||::|| ::||::|| | ::||::|| | ::||::|| | ::||::|| | | ::||::|| | ::||::|| | ::||::|| | ::||::|| | ::||::|| | ::||::|| | ::||::|| | ::||::|| | ::||::|| | ::||::|| | ::||::|| | ::||::|| | ::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::|::|::|::|::|::|::|::|::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGTCIPNAVEVSVPLKLYCNGDGEWMVPVGACTCAAGYEPAMKDTQCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGSCVNNSKEEDPP-RMYCSTEGEWLVPIGKCSCNAGYEE--RGFMCQ
                                                                                                                                                                                                                   108;
                                                                                                                                                                                                               Similarity 49.8
08; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity 51.:
17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              ::104770; Ephb3:
PS00790; RECEPFOR_TYR_KIN_V_1;
PS00791; RECEPFOR_TYR_KIN_V_2;
PS00107; PROTEIN_KINASE_ATP; 1
PS00109; PROTEIN_KINASE_TYR; 1
                                                                                                                                                                                                                                                                                                         938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                         103996
                                                                                                                                                                                                                                49.18;
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51.3%;
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                                                                                                                                                                                                                                                                                                         MW;
                                                                                                                                                                                                                   45;
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -HGVKEREHQFTKIDTIAADESFTQMDLGDRILKLNTE
                                                                                                                                                                                                             Score 589; DB 11;
Pred. No. 1.7e-49;
5; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 644; DB 13;
Pred. No. 7.1e-55;
8; Mismatches 51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                         2B01D2A0 CRC32;
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Mus.
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176
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C -1- SIMILARITY: TO OTHER PROTEIN TYROSINE KINASES IN THE CATALYTI CONTAINS TO THE EMPRIN TECEPTOR FRAILY.

C -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

C -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

FEMBL; L143621; AAA93527.1; -.

REMBL; L143621; AAA93527.1; -.

REMBL; L143621; AAA93527.1; -.

REPROSITE; PS00109; PROTEIN_KINASE_ATP; 1.

REPROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

REPROSITE; PS00109; RECEPTOR_TYR_KIN_V 1; 1.

REPROSITE; PS00791; RECEPTOR_TYR_KIN_V 2; 1.

REPRAM; PF00041; fn3; 2.

REPRAM; PF00041; fn3; 2.

REPRAM; PF000536; SAM; 1.

TENSÉGRAGE: TYROSINGER PROTEIN TYPE III-LIKE DOMAINS.
 Query Match
Best Local Similarity
Matches 102; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q91736;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 12, Last annotation update)
01-NOY-1999 (TREMBLREL. 12, Last annotation update)
EPH RECEPTOR TYROSINE KINASE (XELK) (FRAGMENT).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                              NP_BIND
DISULFID
BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                 DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                              Receptor;
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                                                                                                                                                                                          DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCALES J.B., WINNING R.S., RENAUD C.S., SHEA L.J., "NOVEL members of the eph receptor tyrosine Kinase during Xenopus development."; Oncogene 11:1745-1752(1995).
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                                                                                                                                                                                                                                                                                                        Transferase;
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                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                       TRANSMEM
                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCVNNSKEEDPP-RMYCSTEGEWLVPIGKCSCNAGYE 213 :|: |: | | ::||: :||: | |:| |:| |:| ACIANAYEVSVPLKLYCNGDGEWMVPVGACTCATGHE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96068901.
                                                                                                                                                                                                                                                                                          Transmembrane;
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                                                                                                                                                                                                                                                                                                    Tyrosine-protein kinase;
                                                                ξ,
                                                              398
100850
                                                                                         47.0%;
55.1%;
                                                                                                                                                                                                                                                                                          Glycoprotein;
; Score 563.5; DB 13;
; Pred. No. 5e-47;
42; Mismatches 34;
                                                                ¥.
                                                                                                                        PROTEIN KINASE.

ATP (BY SIMILARITY).

BY SIMILARITY.

ATP (BY SIMILARITY).

BY SIMILARITY.
                                                              POTENTIAL.
POTENTIAL.
W; C096D006
                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL). IG-LIKE C2-TYPE DOMAIN (
                                                                                                                                                                                      FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III.
                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
                                                                                                               PHOSPHORYLATION (AUTO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   902
                                                                                                                                                                                                                                                                                       ATP-binding; Phosphorylation;
; Immunoglobulin domain.
                                                               CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ₽
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                        Length
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                                                                                                               (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             + PROTEIN
                                                                                                                                                                                                                             SIMILARITY).
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 7;
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Best Local Similarity 45.4
Matches 103; Conservative
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Q07494;
01-NOV-1996 (TIEMBLEGL. 01, C
01-NOV-1996 (TIEMBLEGL. 01, L
01-NOV-1999 (TIEMBLEGL. 12, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Noommathae: Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oncogene 8:1807-1813(1993).
EMBL; Z19110; CAAPS26:1; -.
HSSP; P00523; 2PTK.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00536; SAM; 1.
PFAM; PF00069; pkinase;
PFAM; PF01404; EPH_lbd;
PFAM; PF00041; fn3; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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RGTCIPNAEEVDVPIKLYCNGDGEWMVPIGRCTCKAGYEPENNVACR
                                                                                                                                       IREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEV 175
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Last annotation update)
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EPA8_HOUSE
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EPB2_CHICK
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EMBL; AA8003; CAA01906.1; -.
PIR; A38224; A38224.
HSSP; P00523; 2PTK.
MIM; 179611; -.
PRLNTS; PR00104; FNTYPEIII.
PRLNTS; PR00109; TYRKINASE.
PRNSTS; PR00109; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
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Result No.

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35 82.5 6.9 461 1 HMCS_ARATH 36 80 6.7 819 1 EEGG_YEAST 37 79.5 6.6 3106 1 LMA2_MOUSE 38 78.5 6.5 158 1 YKPS_KUULA 39 77.5 6.5 1584 1 DYENS_KUULA 40 77.5 6.4 806 1 SYL_HELDY 41 76.5 6.3 10.46 1 CHID_VIBFU 42 75.5 6.3 10.46 1 CHID_VIBFU 43 74.5 6.2 769 1 ITB2_PIG 44 74.5 6.2 769 1 ITB2_PIG 45 74.5 6.2 771 1 ITB2_MOUSE ALIGNMENTS	
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01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112)
KINASE RECEPTOR REK4).
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DOMAIN
STRAIN-SPRAGUE-DAWLEY;
MEDLINE; 98120505.
Li Y.Y., McTlernan C.F., Feldman A.M.;
"IL-1 beta alters the expression of the r-EphA3 in neonatal rat cardiomyocytes."
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PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2;
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PFAM; PF00041; fn3; 2
PFAM; PF00069; pkinase; 1.
PFAM; PF000636; SAM; 1.
PFAM; PF011404; EPH_1bd; 1.
                                                                                                    SEQUENCE FROM N.A
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Eukaryota; Metazoa; Chordata;
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Sciurognathi; Muridae;
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PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS001186; EGF_2; UNKNOWN_1.
PROM; PF000641; fn3; 2.
PFAM; PF00069; Pkinase; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF01404; EPH_1bd; 1.
                                                                                                                                                                                                                                             ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                               BINDING
BINDING
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DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -<u>i</u>-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Am. J. Physiol. 274:H331-H341(1998).

-i FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMIL EPHRIN-A2, -A3, -A4 AND -A5.

-i CATALUTIC ACTIVITY: ATP + A PROTEIN TYROSINE ~ ADP + PROTEIN TYROSINE PHOSPHATE.

-i SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-i SUBCELLULAR LOCATION: TYPE I MEMBRANE ROTEIN.

-i SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.

-i SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation; Receptor; Transmembrane; Glycoprotein; Signal.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0014; FNTYPEIII. PRINTS; PRO0109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U69278; HSSP; P16109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
  181
                           172
                                                                             112
                                                   121
                                                                                                    51
                                                                                                                               52
                                                                                                                                                                                            Local Similarity
                                                                                                                                          WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL
                       VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV
 NNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
                                                                           VLGTCKETFNLYYMESDDDHGVKFLEHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV
                                                                                                                              WEETSGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL
                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. 274:H331-H341(1998).
RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1FSB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC06273.1; -.
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86
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5 8
8
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CYS-RICH.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                ¥
                                                                                                                                                                                                                                                                                 POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                           Score 1186; DB 1;
Pred. No. 1.1e-101
                                                                                                                                                                                                                                           POTENTIAL.
POTENTIAL.
#; F170C49312F7A0AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      EPHRIN TYPE-A RECEPTOR 3. EXTRACELLULAR (POTENTIAL). POTENTIAL.
                                                                                                                                                                                Mismatches
                                                                                                                                                                                                        Length
                                                                                                                                                                               Indels
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232 NNSKEEDPPRMYCSTEGEWLVPIGKCTCNAGYEERGFICQ 271

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RESULT 3

EPA3_MOUSE
ID EPA3_M
AC P293_M
AC ENASE
GN EPHA3
OS MUS mu
OC EUKARY
OC EUKARY
AC MEDIAIN
RA SAJJAd
RT At lea At lea At lea
RT AT AT lea
RT AT LEA
                                                                                                                                                                                                                                  PRINTS; PRODOLY; FNYEFIII.

PRINTS; PRODIO9; TYRKINASE_ATP; 1.

PROSITE; PSODIO9; PROTEIN_KINASE_ATP; 1.

PROSITE; PSODIO9; PROTEIN_KINASE_TYR; 1.

PROSITE; PSODIO1; PROTEIN_KINASE_DOM; 1.

PROSITE; PSODO790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PSODO791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PSODO186; EGF_2; UNKNOWN_1.

PROM; PFO0041; fn3; 2.

PFAM; PFO0065; SAM; 1.

PFAM; PFO00536; SAM; 1.

PFAM; PFO00536; SAM; 1.
     DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                          Receptor;
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-1992 (Rel. 24, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M68513; AAA39521.1; EMBL; M68515; AAA39522.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     at least two forms of the receptor."; New Biol. 3:769-778(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; >2001470.
Sajjadi F.G., Pasquale E.B., Subramani S.;
Identification of a new eph-related receptor tyrosine kinase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE; 92031278.
Sajjadi F.G., Pasquale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KINASE RECEPTOR ETK1) (MEK4).
EPHA3 OR ETK1 OR MEK4 OR TYRO4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A45583; A45583.
HSSP; P16109; 1FSB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGD; MGI:99612; EPHA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHREN-A2, -A3, -A4 AND -A5.
CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +
PROTEIN TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: A SECRETED VARIANT WITHOUT THE TRANSMEMBRANE REGION AND THE KINASE DOMAIN IS PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: GREATEST LEVELS OF EXPRESSION OCCURRING IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rodentia;
                                                                                                                                                                                          Transmembrane;
                      Tyrosine-protein kinase; ATP-binding; Phosphorylation; cansmembrane; Glycoprotein; Signal; Alternative splicing a BY SIMILARITY.

21 983 EPHRIN TYPE-A RECEPTOR 3.
21 540 EXTRACELLULAR (POTENTIAL).

541 564 POTENTIAL.
555 983 CYTOPLASMIC (POTENTIAL).

21 320 CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS WEBSTER;
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     983
540
564
983
320
431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ALT_SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-EMBRYO
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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  (EC 2.7.1.112) (TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
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A3_CHICK

C P2931B;
C P2931B;
T 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update
DT 01-NOV-1997 (Rel. 35, Last annotation upda
DE EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.

DE KINASE RECEPTOR ETK1) (CEK4).
GN EPHA3 OR ETK1 OR CEK4
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata;
Nacquathae; Galliformes; Phasianidae; P
                                                                                               X MEDLINE; 92031278.

RA Sajjadi F.G., Pasquale E.B., Subramani S.;

RT Tidentification of a new eph-related receptor tyrosine kinase gene from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor.";

RL New Biol. 3:769-778(1991).

CC -i- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO CC -i- FUNCTION. RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO CC -I- CATALYTIC &CTIVITY: ATP + A PROTEIN TYROSINE - ADP + CC CATALYTIC &CTIVITY: ATP + A PROTEIN TYROSINE - ADP + CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

CC -I- TISSUE SPECIFICITY: GREATEST LEVELS OF EXPRESSION OCCURRING IN THE CATALYTIC
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Best Local :
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          This SWI
between
the Eurc
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VARSPLIC
SEQUENCE
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MOD_RES
CARBOHYD
CARBOHYD
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CARBOHYD
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NP_BIND
BINDING
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE; 92031278.
                                                                       -i- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CAT.

DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.

-i- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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          tween the Swiss Institute of Bioinf
European Bioinformatics Institute.
by non-profit institute.
                                SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NNSKEEDPPRMYCSTEGEWLVPIGKCTCNAGYEERGFICQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VIGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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882
653
653
746
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779
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492
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98.6%;
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          institutions as long
                                                                                                                                                                                                                                                                                                              data; Craniata; Vertebrata;
Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (BY SIMILARITY).

BY SIMILARITY.

PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

BE44A6655D8107A2 CRC64;
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Pred. No. 8.3e
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                      update
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C 2.7.1.112)
          There are no rest
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3.3e-101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270
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                                                                                                                                                                                                                                                                                                                                                                              (TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                            Archosauria;
                     restrictions
                                    EMBL
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                                   a collaboration - MBL outstation
                                                                                                                                                                                                                                 encodes
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RESULT
EPA6_R
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Best Local Similarity
Matches 208; Conserv
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PRINTS; PR00109; TYRKINASE.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS001186; EGC=PTOR_TYR_KIN_V_2; 1.

PROSITE; PS01186; EGC=PTOR_TYR_KIN_V_2; 1.
       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update
EPHRIN TYPE-A RECEPTOR 6 PRECURSOR (EC 2.7.
KINASE RECEPTOR EHK-2) (EPH HOMOLOGY KINASE
EPHA6 OR EHK2 OR EHK-2.
                                                                                                  EPA6_RAT P54758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transferase;
Receptor; Tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
NP_BIND
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ACT_SITE
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                                                                                                                                   RAT
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TRANSMEM
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or send a
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DOMAIN
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PFAM;
PFAM;
Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M68514;
PIR; B45583; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                      181
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                                                                                                                                                                                                                                                                                                        NNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
                                                                                                                                                                                                                                                                GPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCV
                                                                                                                                                                                                                                                                                                                                                                 WEEISGVDEHYTPIRTYQESNVMDHSQNNWLRTNWIPRNSAQKIYVELKFTLRDCNSIPL
                                                                                                                                                                                                                                                                                                                                                                                     WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL 60
                                                                                                                                                                                       NHSKEEEPPKMYCSTEGEWLVPIGKCLCNAGYEERGFACQ
                                                                                                                                                                                                                                               GPVSKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00041; fn3; 2.
PF00069; pkinase; 1.
PF00536; SAM; 1.
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norvegicus
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an email t
                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                  STANDARD;
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license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                          94.98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MW;
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CYTOPLASMIC (POTENTIAL,
CYS-RICH.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1139; I
Pred. No. 2.4e
6; Mismatches
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POTENTIAL.
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                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E8895F0BDF77651E CRC64;
                    ion update)
(EC 2.7.1.112) (TYROSINE-PROTEIN
GY KINASE-2).
                                                                                                               948
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2.4e-97;
hes 6;
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Best Local
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PRINTS; PRO0109; TYRKINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00701; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              malsonplerre P.C., Barrezueta N.X., Yancopoulos G.D.,
"Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine kinase family with distinctive structures and neuronal expression oncogene 8:3277-3288(1993).
                                                                                                                                                                                                                                                                                                                  DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
NP_BIND
NP_BIND
ACT_SITE
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: TIVE I DEFINITION OF THE PROTEIN-TYROSINE KINASES IN DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00041; fn3; 2.
PFAM; PF00069; pkinase; 1.
PFAM; PF01404; EPH_lbd; 1.
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY.
-1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P00523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                            180
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                                                                                                                                                                           116
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                                                                                                                                                      121
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SUBCELLULAR LOCATION: TYPE I MEMBRANE
                                                                                                                                                                       VNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEE
                                                                                                                              VKSSEERDTPKLYCGADGDWLVPLGRCICTTGYEE
                                                                                                                                                                                                                                                               al Similarity
159; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane;
                                                                                                                                                                                                                                                               Conservative
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                                 STANDARD;
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                                                                                                                                                                                                                                                                       76.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; POTENTIAL
                                                                                                                                                                                                                                                                                                                    MW;
                                                                                                                                                                                                                                                                                                                           EPHRIN TYPE-A RECEPTOR 6.
EXTRACELLUAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
PROTEIN KINASE.
AIP (BY SIMILARITY).
AIP (BY SIMILARITY).
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                            Score 914.5; DB 1;
Pred. No. 1.2e-76;
"""matches 24;
                                PRT;
                                                                                                                                                                                                                                                                                                                   A47DC78EDB2DEF30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal.
                                ξ
                                                                                     270
                                                                                                          214
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                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THE CATALYTIC
                                                                                                                                                                                                                                                                                   948;
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                    179
                                                                                                                                                                                                                   115
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Query Match
Best Local Similarity
Matches 159; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1;
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2;
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROM; PF00041; fn3; 2.
PFAM; PF00069; pkinase; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF01404; EPH_lbd; 1.
                                                                                                                                                                                                                  DOMAIN
NP_BIND
BINDING
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lee A.M., Navaratnam D., Ichimiya S., Greene M.I., Davis J.G.; "Cloning of m-ehk2 from the murine inner ear, an eph family receptyrosine kinase expressed in the developing and adult cochlea."; DNA Cell Biol. 15:817-825(1996).

-i- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U58332; AAB53836.1; -. HSSP; P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
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EPHRIN TYPE-A RECEPTOR 6 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK-2) (EPH HOMOLOGY KINASE-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPHRIN-A1, -A2, -A3, -A4 AND -A5
-I- CATALTTIC ACTIVITY: ATP + A PROTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPHA6 OR EHK2 OR EHK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00014; FNTYPEIII.
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 97047913.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
    61
                                          56
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATI
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGI:10803
VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV
                                      WDAITEMDEHNRPIHTYQVCNVMEPNQNNWLRTNWISRDAAQKIYVEMKFTLRDCNSIPW
                                                          WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRO0014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane;
                                                                                                                                                                                                                    23
550
571
636
636
662
797
797
797
1035
                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tyrosine-protein kinase; ATP-binding; Phosphorylation;
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549
570
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943
644
662
797
342
396
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RECEPTOR_TYR_KIN_V_1;
RECEPTOR_TYR_KIN_V_2;
                                                                                                                                     76.2%;
74.0%;
                                                                                                                                                                                                                    116137
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein;
POTENTIAL.
                                                                                                                                                                                                                  POTENTIAL.
POTENTIAL.
MW; 560B264
                                                                                                                                     Score 914.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                              BY SIMILARITY.
                                                                                                                                                                                                                                                                                                               ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
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                                                                                                                     Mismatches
                                                                                                                                                                                                                560B264194A5EF74 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                     1.3e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal.
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RESULT 7
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                            PRINTS; PRO0014; FNTYPEIII.

PRINTS; PRO0109; TYRKINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS007091; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS007901; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS001186; EGF_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; D38174;
EMBL; Z19059;
HSSP; P00523;
                                                                                                                                                                                                                               This SWIS between
  PFAM;
PFAM;
PFAM;
                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                            Oncogene 8:1807-1813(1993).

-!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY.
-!- EPHRIN-A1, -A4 AND -A5. BINDS MORE POORLY TO EPHRIN-A2
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                 Sajjadi F.G., Pasc
"Five novel avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-SPINAL CORD;
                                                                                                                                                                                                                                                                                                    ÷
                                                                                                                                                                                                                                                                                                                                                                     expressed
                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                              <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ando M., Tanaka H
                                                                                                                                                                                                                                                                                                                                                                                                                                                             undo M., Tanaka n.,
"The receptor tyrosine kinase,
"The receptor tyrosine kinase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176
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                                                                                                                                                                                                                                                               SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPIERKGFYLAFQDIGACIALVSVRVFYKKCPFTVRSLAMFPDTIPRVDSSSLVEVRGSC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                 OF
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Nakamura M.,
                                                                                                                                                                                                                                                                                                                                                                                                        93288394.
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                                                                                                                                                                                                                                                                                                                                                                                                                              138-986 FROM N.A.
                                                                                                                           ; BAA07373.1; -.; CAA79509.1; -.
fn3; 2.
pkinase;
SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                             Pasquale
                                                                                                                                                                                                                                                                                                                                                                                 quale E.B.;
Eph-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hirokawa
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THE CATALYTIC
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RESULT 8
EPA4_HUMAN
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Best Local S
Matches 162
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DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
NP_BIND
BINDING
BIND
RES
CARBOHYD
CARBOHYD
CARBOHYD
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                            Fox G.M., Holst P.L., Chute H.T., Linc
Basu R., Welcher A.A.;
"cDNA cloning and tissue distribution
protein tyrosine kinases.";
Oncogene 10:897-905(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor;
SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                    EPA4_HUMAN STANDARD; PRT; 986 AA.
p54764;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR SEK) (RECEPTOR PROTEIN-TYROSINE KINASE HEK8).
EPHA4 OR SEK OR HEK8.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                   TISSUE-BRAIN;
MEDLINE; 95206782.
Fox G.M., Holst P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase;
                                                                                                                                                                                                                                                                                            Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  μ.
FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. EPHRIN-A1, -A4 AND -A5. BINDS MORE POORLY TO EPHRIN-A2 CATALYTIC ACTIVITY: ATF + A PROTEIN TYROSINE - ADF + PROTEIN TYROSINE PHOSPHATE.

SUBJECTIOUR TO THE PROTEIN TYPE I MEMBRANE PROTEIN.

SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAIN SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
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162; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF01404; EPH_lbd; 1.
ferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                            Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.98;
73.38;
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POTENTIAL
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ATP (BY SIMILARITY).

BY SIMILARITY.

PHOSPHORYLATION (AUTO-) (POTENTIAL).

POTENTIAL.

POTENTIAL.

POTENTIAL.

R -> G (IN REF. 2).

S -> T (IN REF. 2).

S -> T (IN REF. 2).
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Pred.
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CYTOPLASMIC (POTENTIAL).

FIBRONECTIN TYPE-III (BY

FIBRONECTIN TYPE-III (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -> G (IN REF. 2).
-> T (IN REF. 2).
BD88C2A5BD840A0F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'EIN KINASE.
(BY SIMILARITY).
(BY SIMILARITY).
                                                                                                                                                                                                   Lindberg R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    910.5;
No. 2.
                                                                                                                                                                 of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1,
2.9e-76;
28;
                                                                                                                                                               five
                                                                                                                                                               human
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   DOMAINS.
THE CATALYTIC
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SIMILARITY).
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AND A-3.
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                                                                                                                                                               receptor
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BABAB
                                                       RESULT 9
EPA4_MOUSE
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Best Local Similarity
Matches 162; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L36645; AAA74246.1; -.

HSSP; P00523; 2PTK.

MIM; 602188; -.

PRINTS; PRO0014; FNTYPEIII.

PRINTS; PRO00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

PFAM; PF00041; fn3; 2.

PFAM; PF00040; fn3; 2.

PFAM; PF000516; SAM; 1.

PFAM; PF001404; EPH_1bd; 1.

PFAM; PF01404; EPH_1bd; 1.
EPA4_MOUSE
Q03137;
Q1-OCT-1994
Q1-OCT-1994
Q1-NOV-1997
                                                                                                                                                                                                                                                                                                                                 TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
NP_BIND
BINDING
ACT_SITE
MOD_RES
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                   234
                                                                                                                       180
                                                                                                                                             174
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                                                                                                                                                                                                                                            WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL 60
                                                                                                                                          VNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
                                                                                                  VNNSEEKDVPKMYCGADGEWLVPIGNCLCNAGHEERSGECQ
                                                                                                                                                                                                                                  WEEVSIMDEKNTPIRTYQVCNVMEPSQNNWLRTDWITREGAQRVYIEIKFTLRDCNSLPG 113
 (Re1.
(Re1.
(Re1.
                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                             Ą,
                                            STANDARD;
 30,
35,
                                                                                                                                                                                                                                                                                        75.5%;
73.3%;
                                                                                                                                                                                                                                                                                                                                    109859
                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein;
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                   ¥.
                                                                                                                                                                                                                                                                             30;
                                                                                                                                                                                                                                                                           Score 905.5;
Pred. No. 8.2e
30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III (BY
FIBRONECTIN TYPE-III (BY
                                                                                                                                                                                                                                                                                                                                POTENTIAL.
v; 0C39C1152EDDD46F CRC64;
                                                                                                                                                                                                                                                                                                                                                      PHOSEHORYLATION (AUTO-) (POTENTIAL).
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPHRIN TYPE-A
EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                        No. 8.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal.
                                                                                                                                                                                                                                                                     , DB 1,
d.2e-76;
28;
                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RECEPTOR 4. (POTENTIAL)
                                                                                                                      220
                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                   986;
                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                           Gaps
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Last sequence up

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DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DOMAIN
NP_BIND
                                                                                                                                                                            PRINTS; PRO0014; ENTYPEIII.

PRINTS; PRO0109; TYRKINASE ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstatithe European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commendations of the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 93205393.

Gilardi-Hebenstreit P., Nieto M.A., Frain M., Chestier A., Wilkinson D.G., Charnay P.;
Oncogene 8:1103-1103(1993).

-I- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHI
                                                                                                                                PFAM; PF00041; fn3; 2.
PFAM; PF00069; pkinase; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF01404; EPH_lbd; 1.
                                                                                                                                                                                                                                                                                 EMBL; X65138; CAA46268.1; -.
EMBL; X57241; CAA40517.1; -.
EMBL; S57168; AAB25836.1; -.
HSSP; P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "An Eph-related receptor protein tyrosine kinase expressed in the developing mouse hindbrain."; oncogene 7:2499-2506(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gilardi-Hebenstreit P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-C57BL; TISS
MEDLINE; 93096484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPHRIN
KINASE
                                                                                                 Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                       entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chestier A., Wilkinson D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Rodentia; Sciurognathi; Murid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse),
Mus musculus (Mouse),
Chordata;
                                                                                                                        Transferase;
                                                                                                                                                                                                                                                                      MGD; MGI:98277; EPHA4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A1, -A4 AND -A5. BINDS MORE POORLY TO EPHRIN-A2 AND A-3 MAY PLAY A ROLE IN A SIGNAL TRANSDUCTION PROCESS INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN RECEPTOR SEK) (MPK-3).
  548
570
5325
436
621
                                                                                                                       Tyrosine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-EMBRYONIC
  19
986
986
569
986
435
532
635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nieto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .G.,
                                                                                                          Glycoprotein;
           EPHRIN TYPE-A RECEPTOR 4.
EXTRACELULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III (BY SIMILARITY).
FIBRONECTIN TYPE-III (BY SIMILARITY).
PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Charnay P.;
                                                                                                POTENTIAL
                                                                                                      kinase; ATP-binding; Phosphorylation; pprotein; Signal; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            niata; Vertebrata;
Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Frain
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THE CATALYTIC
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RESULT
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Best Local S
Matches 160
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MOD_RES
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VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK-1) (EPH HOMOLOGY KINASE-1) (BRAIN-SPECIFIC KINAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
                       use by non-profit institutions as long modified and this statement is not removed: entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                             Zhou R., Copeland T.D., Kromer L.F., Schulz N.T., "Isolation and characterization of Bsk, a growth factor receptor-like tyrosine kinase associated with the limbic system.";
J. Neurosci. Res. 37:129-143(1994).
                                                                                                                                                                                                                                                                                                 STRAIN-BALB/C; TI
MEDLINE; 94194581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q60629;
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                                                                                                                                                                                                                                    J. Neurosci. Res.
                                                                                                                                                                                                                                                                                                                                                          Eutheria;
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                EPHA5 OR EHK1 OR CEK7 OR BSK.
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       234
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                                                                                                                    SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY. SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOME
                                                                                                                                                                                                       FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. EPHRIN-A1, -A2, -A3, -A4 AND -A5.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
                                                                                                                                                                  PROTEIN TYROSINE PHOSPHATE. SUBCELLULAR LOCATION: TYPE TISSUE SPECIFICITY: BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                 musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VLGTCKETF%LYIMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VMGTCKETFNLYYYESDNDKERFIRESQFGKTDTIAADESFTQVDIGDRIMKLNTEIRDV
U07357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                       Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    986
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                                                                                                                                                                                                                                                                                                                  TISSUE-BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
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423
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Pred. No. 1.3e
30; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
MISSING (IN SHORT ISOFORM).
J D16AD8B85668C80E CRC64;
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                                (See http://www.isb-sib.ch/announce/
                                                        There are no restrictions ong as its content is in
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-74;
                                                                                                                            III-LIKE DOMAIN.
                                               Usage
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Best Local S
Matches 151
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PRINTS; PRO0109; TYRKINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
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BINDING
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CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                             PPAS_RAT STANDARD; PRT; 1005 AA. P54757; PCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) KINASE RECEPTOR EHK-1) (EPH HOMOLOGY KINASE-1). EPHAS OR EKH1 OR EHK-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor;
Maisonpierre P.C., Barrezueta N.X., Yancopoulos G.D.; "Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosin kinase family with distinctive structures and neuronal expression."; Oncogene 8:3277-3288(1993).
                                                                                  STRAIN-SPRAGUE-DAWLEY; MEDLINE; 94067777.
                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
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                                                                                                                                                                       Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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                                                                                                                             SEQUENCE FROM N.A.
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151; Conservative
                                                                                                                                                                       Rodentia;
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SAM; 1.
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                                                                                                                                                                   Sciurognathi;
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68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e; Glycoprotein; Signal.

BY SIMILARITY.
EPHRIN TYPE-A RECEPTOR 5.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
                                                                                                         TISSUE-BRAIN,
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Pred. No. 2.8e
35; Mismatches
                                                                                                                                                                                           Craniata;
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                                                                                                                                                                     Muridae;
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ae; Murinae;
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                                      Eph receptor-like tyrosine
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PRINTS; PRO0109; TYKKINASE_ATP; FJ
PROSITE; PS00107; PROTEIN_KINASE_TYR; 1
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_1;
PROSITE; PS001186; EGF_2; UNKNOWN_1.
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SEQUENCE FROM N.A.
SERAIN-SPRAGUE-DAWLEY; T
MEDLINE; 95206467.
MEDLINE; Pfart S., Mi
  CONFLICT
CONFLICT
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CARBOHYD
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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"Expression and developmental regulation of Ehk-1,
Elk-11ke receptor tyrosine kinase in brain.";
Neuroscience 63:163-178(1994).
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HSSP; P00523;
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TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED SYSTEM. PREDOMINANTLY EXPRESSED IN NEURONS.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARI
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CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE
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PF00069;
PF01404;
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PROTEIN_KINASE_DOM; 1.
RECEPTOR_TYR_KIN_V_1;
RECEPTOR_TYR_KIN_V_2;
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POTENTIAL
SPLICED FORMS).
SGSCCEGGGGRASSLCAVAHPSLIW -
SPLICED FORMS).
D -> E (IN REF. 2).
G -> A (IN REF. 2).
G -> A (IN REF. 2).
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
POTENTIAL.
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SPLICED FORMS)
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SEQUENCE
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
KINASE RECEPTOR EHK-1) (EPH HOMOLOGY KINASE-1) (RECEPTOR PROTEIN-
TYROSINE KINASE HEK7).
           This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI the European Bioinformatics Institute. There are no restricuse by non-profit institutions as long as its content is
                                                                                                                                                                                                                 "cDNA cloning and tissue distribution protein-tyrosine kinases."; Oncogene 10:897-905(1995).
                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
Eukaryota; Metazoa; (
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Fox G.M., Holst P.L.,
                                                                                                                                                                                                                                                                                        TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                   SEQUENCE OF 25-1037 FROM
                                                                                                                                                                                                                                                                                                                         Submitted (JAN-1996) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                       Miescher
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                                                            SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATA DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                     SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE
ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESS
                                                                                                                                                                 EPHRIN-A1, -A2, -A3, -A4 AND -A5.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE PROTEIN TYROSINE PHOSPHATE.
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MOUSE STANDARD; PRT; C61772; Q61773; Q61774; Q61505; Q61772; Q61773; Q61774; Q61505; Q61772; Q61773; Q61774; Q61505; Q61772; Q61773; Q61774; Q61505; Q1-NOV-1997 (Rel. 35, Last sequence update) Q1-NOV-1997 (Rel. 35, Last annotation update) Q1-NOV-1997 (
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PROSITE; PS00790; RECEPTOR_TVR_KIN_V_1;
PROSITE; PS00791; RECEPTOR_TVR_KIN_V_2;
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PFAM; PF00041; fn3; 2.
PFAM; PF00069; Pkinase; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF00404; EPH_bd; 1.
PFAM; PF01404; EPH_bd; 1.
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HSSP; P00523;
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AAA74245.
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); PROTEIN_KINASE_TYR; 1.
l; PROTEIN_KINASE_DOM; 1.
l; RECEPTOR_TYR_KIN_V_1; 1.
l; RECEPTOR_TYR_KIN_V_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYRKINASE.
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POTENTIAL.
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Pred. No. 1.2e
95; Mismatches
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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POTENTIAL.
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EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
.2e-71;
nes 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RECEPTOR 5. (POTENTIAL).
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Alternative splicing
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PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00799; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PF0M; PF00041; fn3; 2.
PFAM; PF00041; fn3; 2.
PFAM; PF000536; SAM; 1.
PFAM; PF00536; SAM; 1.
                                             DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clossek T., Millauer B., Ullrich A.;
"Identification of alternatively spi
MDK1, a novel receptor tyrosine kina
nervous system.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBI
                                                                                                                                          Transferase;
                                                                                                                                                                                                                                                                                                                 MGD; MGI:95276; EPHA7.
PRINTS; PRO0014; FNTYPEIII.
PRINTS; PR00109; TYRKINASE.
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[2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Eutheria; Rodentia; Sciurognai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 96081374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MDK1.

TISSUE SPECIFICITY: WIDELY EXPRESSED IN EMBRYO. IN ADULT, EXPRESSION RESTRICTED TO HIPPOCAMPUS, TESTIS AND SPLEEN. EXPRESSION FOR PROTEIN-TYROSINE KINASES IN THE CATAL DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.

SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BE EPHRIN-A1, -A2, -A3, -A4 AND -A5.

EPHRIN-A1, -A2, -A3, -A4 AND -A5.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.

PROTEIN TYROSINE PHOSPHATE.

SUBCELLULAR LOCATION: TYPE I MEMBERS OF THE PROTEIN (MDK1, MI ALTERNATIVE PRODUCTS: FIVE FORMS OF THE PROTEIN (MDK1, MI MDK1-2, MDK1-TAD MDK1-T2) ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. THE SEQUENCE SHOWN HERE IS THE SPLICING OF THE SAME GENE. THE SEQUENCE SHOWN HERE IS THE
                                                                                                                                                                                                                                                                                                                                                                   X79082; CAA55687.1; -.

X79083; CAA55688.1; -.

X79084; CAA55689.1; -.

X81466; CAA57224.1; -.

P00523; 2PTK.
                                                                                                                           Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431-998 FROM N.A.
                                                                                                                    Tyrosine-protein kinase; ATP-binding; Phosphorylation; ansmembrane; Glycoprotein; Signal; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               V.A., AND ALTERNATIVE TISSUE-BRAIN;
998
556
577
998
438
537
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                                                                                                         Glycoprotein;
POTENTIAL.
        EPHRIN TYPE-A RECEPTOR 7.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata;
chi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ISOFORM MDK1).
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murine
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Best Local S
Matches 156
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EPA7_HUMAN
Q15375;
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
EPHRIN TYPE-A RECEPTOR 7 PRECURSOR (EC 2.7.1.11
KINASE RECEPTOR EHK-3) (EPH HOMOLOGY KINASE-3)
TYMOSINE KINASE HEKIL).
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CARBOHYD
VARSPLIC
VARSPLIC
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MOD_RES
CARBOHYD
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                                                                                                                                                                                                                                                Fox G.M., Holst P.L.,
Basu R., Welcher A.A.
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
Eukaryota; Metazoa; (
Eutheria; Primates; (
                                                                                                                                                                                                                                                                                                                                                                                                                    TYROSINE KINASE HEK11).
EPHA7 OR EHK3 OR HEK11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                       MEDLINE; 95206782
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                                                                                                                                                                                                                                                                                                          'ISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                        EQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               998
480
111874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        998
626
                                                                                                                                                                                                                                                                                                                                                         Chordata; Craniata; Ve
Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71
                                                                                                                                                                                                                                                                 Chute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Æ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MISSING (IN ISOFORM MDK1-1).

MISSING (IN ISOFORM MDK1-2).

FKFPGTKTYID -> SLYTNEHLSVL (IN :MTK1-T1).

MISSING (IN ISOFORM MDK1-T1).

FKFFGTKTYIDPETYEDPNRAVHQFAK -> :

EKTQHNKKMMIASCSRL (IN ISOFORM MDK1-T2).

Y -> H (IN REF. 2).
                                                                                                                                                                                                                                                               H.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 857.5;
Pred. No. 2.26
%6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -> H (ÎN REF. 2).
81C5538E15AEA2FA CRC64;
                                                                                                                                                                                                                                                                 Lindberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      866
                                                                                                                                                                                                                                                                                                                                                                               Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   es 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
                                                                                                                                                                                                                                                                 R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .112) (TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (RECEPTOR
                                                                                                                                                                                                                                                                 Janssen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                 Mammalia
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                                                                          CATALYTIC
                                                                                                                                                                                                                                                                 A.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ب
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RESULT EPA7_RAT
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 SGREDITAC
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00107; PROTEIN KINASE_ATP; PROSITE; PS00109; PROTEIN_KINASE_TYR; PROSITE; PS00111; PROTEIN_KINASE_DOM; PROSITE; PS00790; RECEPTOR_TYR_KIN_V_PROSITE; PS00791; RECEPTOR_TYR_KIN_V_PROSITE; PS007186; EGF_2; UNKNOWN_1.
PROM; PF00061; fin3; 2.
PFAM; PF00061; pkinase; 1.
PFAM; PF000536; SAM; 1.
PFAM; PF01404; EPH_1bd; 1.
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
EPHRIN TYPE-A RECEPTOR 7 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK-3) (EPH HOMOLOGY KINASE-3).
EPHA7 OR EHK3. R. ENK-3.
                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
SEQUENCE
                                                                                  EPA7_RAT P54759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its contain modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L36642; AAA74243.1; -. HSSP; P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0109
                                                                                                                                                                                  180
                                                                                                                                                                                                          175
                                                                                                                                                           235
                                                                                                                                                                                                                                121
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                                                                                                                                                                                                                 GPVNKKGEYLAFQDVGACVALVSVRVYEKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSC
                                                                                                                                                                                                                                                                 VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV 120
                                                                                                                                                                                                                                                                                                               WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL
                                                                                                                                                                               VNNSKE---
                                                                                                                                                       VSSAEEEAENAPRMHCSAEGEWLVPIGKCICKAGYQQKGDTCE
                                                                                                                                                                                                                                                     VLGTCKETFNLYYYETDYDTGRNIRENLYVKIDTIAADESFTQGDLGERKMKLNTEVREI
                                                                                                                                                                                                                                                                                                     WEEISGLDENYTPIRTYQVCQVMEPNQNNWLRTNWISKGNAQRIFVELKFTLRDCNSLPG 114
                                                                                                                                                                                                      GPLSKKGFYLAFQDVGACIALVSVKVYYKKCWSIIENLAIFPDTVTGSEFSSLVEVRGTC
                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                 998
                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tyrosine-protein kinase;
                                                                                                                                                                     EDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
                                                                                                                                                                                                                                                                                                                                                                                                                 Ą,
                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN_KINASE_ATP; 1.
PROTEIN_KINASE_TYR; 1.
PROTEIN_KINASE_DOM; 1.
PROCEPTOR_TYR_KIN_V_1; 1
RECEPTOR_TYR_KIN_V_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                              112096 MW;
                                                                                                                                                                                                                                                                                                                                                                 71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein;
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                      37;
                                                                                                                                                                                                                                                                                                                                                   Score 856.5; 1
Pred. No. 2.8e
37; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP (BY SIMILA ATP (BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                       PHOSPHORYLATION (AUTO-) (BY SIMILARITY). POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPHRIN TYPE-A RECEPTOR 7.
                                                                                                                                                                                                                                                                                                                                                                                                               47989CA0D2BB06EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (BY SIMILARITY). (BY SIMILARITY).
                                                                                             998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal.
                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                 .8e-71;
                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                       277
                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     restrictions
                                                                                                                                                                                                                                                                                                                                                                             998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL outstation
                                                                                                                                                                                                                                                                                                                                                   Ψ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'n
                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                           60
                                                                                                                                                                                                      234
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Query Match 71.4
Best Local Similarity 69.4
Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0014; FNTYPEIII.

PRINTS; PRO0109; TYPRINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00701; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS001186; EGF_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                            PROSITE; PS00790; RECEPTOR T
PROSITE; PS00791; RECEPTOR T
PROSITE; PS01186; EGF_2; UNK
PFAM; PF00041; fin3; 2.
PFAM; PF00069; Pkinase; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF01404; EPH_1bd; 1.
                                                                                    MOD_RES
CARBOHYD
CARBOHYD
VARSPLIC
                                                                                                                                   NP_BIND
BINDING
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eutheria;
[1]
                                                                                                                                                                                     DOMAIN
DOMAIN
                                                                                                                                                                                                                         DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U21955;
HSSP; P00523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U21954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Valenzuela D.M., Rojas E., Griffith
ID N.Y., Goldfarb M., Yancopoulos G
"Identification of full-length and
                                                              SEQUENCE
                                                                                                                                                                                                                                                              Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <del>-</del> -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -
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                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: TWO FORMS ARE PRODUCED BY ALTERNATIVE
SPLICING, THE TRUNCATED FORM LACKS THE KINASE DOMAIN. THE LONG
FORM IS MORE WIDELY EXPRESSED IN THE EMBRYO.
TISSUE SPECIFICITY: RESTRICTED TO THE NERVOUS SYSTEM.
SIMILARITY: TO OTHER PROTEIN-TYPOSINE KINASES IN THE CATALYTIC
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPHRIN-A1, -A2, -A3, -A4 AND -A5.
CATALYTIC ACTIVITY: ATP + A PROTEIN
PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FROM N.A.
95249272.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rodentia;
                                                                                                                                                                                                                                                                         Transmembrane;
                                                              998
                                                                                     5578
5578
578
5329
633
7585
7585
7585
7585
                                                                                                                                                                                                                                                          Tyrosine-protein kinase; ATP-binding; Phosphorylation; ansmembrane; Glycoprotein; Signal; Alternative splicing

24 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA86830.1; -.
AAA86831.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2PTK
                                                             Ă,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                             111953
           71.4%;
                                                              MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Griffiths J.
 37;
Score 856.5;
Pred. No. 2.8e
7; Mismatches
                                                                                               POTENTIAL.
POTENTIAL.
                                                          FKFPGTKTYID -> SLVTI
ISOFORM).
N; A7A82A698924876C
                                                                                                                     BY SIMILARITY.
PHOSPHORYLATION (AUTO-)
                                                                                                                                                                                  FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III.
                                                                                                                                                           ATP (BY SIMILAR
                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                   EPHRIN TYPE-A
EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF THE EPHRIN-A FAMILY.
                                                                                                                                               SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYROSINE
DB 1;
2.8e-71;
les 28;
                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Compton
                                                                                    SLYTNEHLSVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ı
                                                            CRC64;
                     Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia;
Rattus.
                                                                                                                      (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ehk-3,
                                                                                    (IN
                        998;
                                                                                                                      SIMILARITY).
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                                                                                                                                                                                                                                                                       splicing
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1 WEEISGYDEHYTPIRTYQYCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL 60

Indels

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Gaps

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Search completed: May 9, 2000, 22:32:06 Job time: 2397 sec

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Result
No.
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Maximum DB seq length: 1000000
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM protein - protein search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9::
   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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904.5
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1: pir1:
2: pir2:
3: pir3:
4: pir4:
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receptor tyrosine kinase Mek4 - mouse

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R;Sajjadi, F.G.; Pasquale, E.B.; Subramani, S.

New Biol. 3, 769-778, 1991

A;Pitle: Identification of a new eph-related receptor tyrosine kinase gene f. A;Pitle: Identification of a new eph-related receptor tyrosine kinase gene f. A;Pastatus: preliminary

A;Reference number: A45583; MUID:92031278

A;Restatus: preliminary

A;Rolecule type: mRNA

A;Residues: 1-983 <SAJ>
A;Residues: 1-983 <SAJ>
A;Cross-references: GB:M68514; NID:g454809; PIDN:AAA48666.1; PID:g211447

A;Cross-references: GB:M68514; NID:g454809; PIDN:AAA48666.1; NCBIP:62411)

C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type: C;Reywords: APP; autophosphorylation; phosphoprotein; transmembrane protein F;619-885/Domain: protein kinase homology <KIN>
F;627-635/Region: protein kinase AIP-binding motif
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C;Species: Gallus g
C;Date: 22-Apr-1993
C;Accession: B45583
C;Accession: FG; Pa
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A;Title: Identification of a new eph-related receptor tyrosine kinase gene f A;Reference number: A45583; MUID:92031278

A;Reference number: A45583; MUID:92031278

A;Recession: A45583

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-983 <SAJ>
A;SCAJ>
A;Cross-references: GB:M68513; NID:g199119; PIDN:AAA39521.1; PID:g199120
A;Note: sequence extracted from NCBI backbone (NCBIN:62398, NCBIP:62401)
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type C:Keywords: ATP: autophosphorylation; phosphoprotein; transmembrane protein F;619-885/Domain: protein kinase homology <KIN>
F;627-635/Region: protein kinase ATP-binding motif
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;Species: Gallus gallus (chicken)
pate: 22-Apr-1993 #sequence_revision 18-Nov-1994
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Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
Accession: A45583
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2; Mismatches
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5; Mismatches 6;
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A;Gene: HEK8
C;Superfamily: protein-tyrosine k
F;619-885/Domain: protein kinase
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A;Residues: 1-948 <MAID
A;Cross-references: EMBL:S68030
C;Superfamily: protein-tyrosine kinase, receptor ty
C;Keywords: ATP; transmembrane protein
F;628-936/Domain: protein kinase homology <KIN>
F;636-644/Region: protein kinase ATP-binding motif
                                                           A;Molecule type: mRNA
A;Residues: 1-986 <RES>
A;Cross-references: GB:L36645;
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A;Accession: S51605
A;Status: preliminary
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A;Title: Ehk-1 and Ehk-2: two novel members
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R; Maisonpierre,
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C;Species: Rattus norvegicus (Norway ra
C;Date: 07-May-1995 #sequence_revision
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74.0%;
                                                            NID:g551613; PIDN:AAA74246.1;
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Pred. No. 2.:
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protein-tyrosine kinase (EC 2.7.1.112) C;Speckes: Mus musculus (house mouse) C;Date: 19-Nov-1997 #sequence_revision C;Accession: $78059; $30505; I58366 R;Charnay, P.
                                                                             RESULT
S78059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: I51549
R; Winning, R.S.; Sargent, T.;
Mech. Dev. 46, 219-229, 1994
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C; Superfamily: protein-tyrosine kinase,
C; Keywords: ATP; transmembrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Pagliaccio, a member of the Eph
A;Reference number: IS1549; MUID:95001564
A;Accession: IS1549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor tyrosine kinase - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996
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A; Residues: 1-985 <WIN>
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No. 1.6e-74;
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No. 1.6e-73;
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C;Superfamily: protein-tyrosine kinase, recept (Keywords: ATP; transmembrane protein F;512-778/Domain: protein kinase homology <KI F;520-528/Region: protein kinase ATP-binding F;801-868/Domain: SAM homology <SAM>
                                                                                                                                                                                                                                                                                                     brain-specific kinase - mouse
C;Species: Mus musculus (house mouse)
C;Date: O2-Jul-1996 #sequence_revision O2-Jul-1996 #
C;Accession: I48967
R;Zhou, R.R.; Copeland, T.D.; Kromer, L.F.; Schulz,
J. Neurosci. Res. 37, 129-143, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Reywords: ATP; autophosphorylation; glycoprotein; phosphopro F;1-15/Domain: signal sequence #status predicted <SIG>F;1-6-986/Product: protein tyrosine kinase Eph #status predicte F;548-569/Domain: transmembrane #status predicted <TMM>F;619-885/Domain: protein kinase homology <KIN>F;619-885/Domain: protein kinase homology <KIN>F;627-635/Region: protein kinase homology ontif F;908-974/Domain: SAM homology <SAM>F;235,340,408,423/Binding site: carbohydrate (Asn) (covalent)
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A;Title: An Eph-related receptor protein
A;Reference number: S30496; MUID:93096484
                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-877 <RES>
A; Cross-references: EMB
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A; Residues: 1-31,55-986 <GIL>
A; Cross-references: EMBL:X65138
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                                                                                                                                                                                                                                                      A; Reference number: I48967; A; Accession: I48967
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                                                                                                                                                      A;Gene: Bsk
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;Keywords: ATP;
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plation; glycoprotein; phosphoprotein;
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 72.2%;
68.3%;
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Pred. No. 2.5e
30; Mismatches
                                                                                                                                                                                   NID:g466369; PIDN:AAA17038.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NID:g54083; PIDN:CAA46268.1; PID:g54084
, M.A.; Frain, M.; Mattei, M.G.; Chestie
 Score
Pred.
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Similarity

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receptor tyrosine kinase - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Species: Natur 1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
C;Accession: $47489
R;Taylor, V; Pfarr, S.; Miescher, G.C.; Honegger, P.; Breitschopf, H.; Lassman submitted to the EMBL Data Library, April 1994
A;Description: Expression and developmental regulation of EHK-1, a neuronal ELK A;Reference number: $47489
A;Reference number: $47489
A;Reference number: $47489
A;Status: preliminary
A;Molecule type: mrNA
A;Residues: 1-898 <TAY>
A;Cross-references: EMBL:X78689; NID:9531543; PIDN:CAA55357.1; PID:9531544
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III
C;Keywords: ATP; transmembrane protein
F;568-834/Domain: protein kinase homology <KIN>
F;576-584/Region: protein kinase ATP-binding motif
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Pred. No. 5.1e
35; Mismatches
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                                   Eph receptor-like
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                       VNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
         VNHSVTDDPPKMHCSAEGEWLVPIGKCMCKAGYEEKNGTCQ
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Oncogene 8, 3277-3288, 1993

A. Pitle: Ehk-1 and Ehk-2: two novel members of the Eph A; Reference number: S49015; MUID:94067777

A. Accession: S51604

A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-981 < MAID:
A; Cross-references: EMBL:S68029

A; Cross-references: EMBL:S68029

A; Note: the authors translated the codon GAC for resid C; Superfamily: protein-tyrosine kinase, receptor type C; Keywords: ATP; transmembrane protein
F; 651-917/Domain: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-893 <mAIS
A; Cross-references: EMBL:S58028
A; Oote: the authors translated the codon GAC for
C; Superfamily: protein tyrosine kinase, receptor
C; Keywords: ATP; transmembrane protein
F; 563-889/Domain: protein kinase ATP-binding moti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               receptor-like tyrosine kinase Ehk-1 - rat C;Species: Rattus norwegicus (Norway rat) C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change C;Accession: S51604 R;Maisonpierre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D. oncogene 8, 3277-3288, 1993
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||||||||:|| ||||::| :::|: ||||||||::|||||::|||||::||
GLGTCKETFNMYYFESDDENGRNIKDNQYIKIDTIAADESFTELDLGDRVMKLNTEVRDV 204
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67.9%;
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Pred. No. 1.1e
36; Mismatches
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Pred. No. 9.5e
36; Mismatches
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67.9%;

Pred. No.

2e-70;

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RESULT 12
$49015
receptor tyrosine kinase Ehk-1 - rat
receptor tyrosine kinase Ehk-1 - rat
c:Species: Rattus norvegicus (Norway rat)
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999
C:Cate: 14-Jul-1995 #sequence_revision exit type in the type: mRNA
A:Cross-references: EMBL:568024
A:Cross-references: EMBL:568026
A:Cross-references: EMBL:568026
A:Cross-references: EMBL:568026
A:Coss-references: EMBL:568026
A:Cross-references: EMBL:568026
A:Coss-references: EMBL:
                                                                                                                                                                                            receptor protein-tyrosine kinase - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 18-C:Caccession: I78843
R:Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.
Oncogene 10, 897-905, 1995
A:Title: CDNA cloning and tissue distribution of five human EPH-likentification of the human EPH-
A:Gene: HEK7
C:Superfamily: protein-tyrosine kinase,
F:627-893/Domain: protein kinase homolog
F:916-982/Domain: SAM homology <SAM>
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Query Match

Score

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A:Experimental source: embryo
C:Comment: This enzyme plays a regulatory role during neural c:Comment: This enzyme plays a regulatory role during neural c:Comment: This enzyme plays a regulatory role during neural c:Comment: bis enzyme plays a sequence #status predicted <SIG>F:J-30/Domain: signal sequence #status predicted <EXT>F:J1-605/Product: receptor tyrosine kinase Ebk-tdl #status preficted <EXT>F:J1-548/Domain: extracellular #status predicted <EXT>F:J31-548/Domain: fibronectin type III repeat <ENI>F:J41-534/Domain: fibronectin type III repeat <ENI>F:J41-534/Domain: transmembrane #status predicted <TMM>
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C;Species: Mus musculus (house mouse)
C;Date: 02-U1-1996 #sequence_revision
C;Accession: I48612; S51741
R;Ciossek, T; Millauer, B.; Ullrich, A
Oncogene 9, 97-108, 1995
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A; Fittle: Identification of alternatively spliced mrnaa encoding variants of MDK1, a nove A; Reference number: 148611
A; Accession: 148612
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Canal Status: preliminary; translated from GB/EMBL/DDBJ
A; Residues: 1-610 <RES>
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Maximum

Searched:

Sequence:

Title:

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8

45	44	43	42	41	40	39	38	37	36	35
460	460	460	466	466	466	466	466	466	466	466
38.3	38.3	38.3	38.8	38.8	38.8	38.8	38.8	38.8	38.8	38.8
1021	1006	1006	987	987	987	987	987	972	972	522
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w70526	W70525	W72256	W11304	W06335	R94652	R89263	R85930	W06331	R76468	W11303
thymus	Human thymus recep	Human receptor typ	Receptor-type tyro	Full length recept	Receptor type tyro	Human non-differen	Protein tyrosine-k	Full-length recept	Mature non-differe	Receptor-type tyro

ALIGNMENTS

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Receptor-type tyrosine kinase reactive with monoclonal antibody III-A4 - is EPH-ELK-like kinase, useful for phosphorylating proteins in modulating pre-B, B and T cell function, in cancer therapy etc.

Claim 6; Fig 1; 58pp; English.

This sequence represets human eph/elk-like kinase (HEK). HEK is expressed in both pre-B cells and T cell lines and in a number of tumours of human origin, eg. lymphoid tumours LKG3, Lila-l and JM, and the epithelial tumour HeLa. This receptor-type thymiddine kinase (TK) and/or its ligands are useful as agents in modulation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HEK polypeptide.

Primer; expression vector; extracellular domain; human; HEK; peh/elk-like; kinase; pre-B; cell; T; tumour; lymphoid; LK63; Lila-1; JM; epithelial; HeLa; receptor-type; thymidine kinase; TK; ligand; B;cellular response; growth; differentiation.
                                                                                                                                                                                                          (HALL-) HALL INST MEDICAL I
Boyd AD, Simpson R, Ward
WPI; 93-036373/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R31466 standard; Protein;
R31466;
24-MAY-1993 (first entry)
                                                                                                                                                                                             P-PSDB; R31466.
                                                                                                                                                                                                                                                             19-JUN-1992; AU0294.
21-JUN-1991; AU-006841.
12-DEC-1991; AU-009992.
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Eph-related
Cek4; Eph; p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus sp.
WO9515375-A.
08-JUN-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 85-89; 129pp; English.
Probes derived from the EPH-related PTKs Cek4 (090659) and Ce (090660) were used to isolate novel cDNA clones (090652-58, 090661-62) from chicken embryo and embryonic brain libraries. Cek4 is highly expressed in the chicken developing brain and embryonic tissues and also in the adult brain and retina. Sequence 983 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-SEP-1994; U10140.
03-DEC-1993; US-162809.
(LJOL-) LA JOLLA CANCER RES
Pasquale EB, Sajjadi FG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             production and/or function analogues have activity in cellular responses such as Sequence 983 AA;
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WPI; 95-215256/28.
N-PSDB; Q90659.
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ilarity 94.1%;
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7; Mismatches 6;
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Pred. No. 7.8e-119;
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Query Match
Best Local Sim
Matches 159;
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US5843749-A.
US5843749-A.
US-D40-1995; 469537.
17-MAR-1995; US-406247.
17-MAR-1995; US-736559.
26-JUL-1991; US-736559.
26-OCT-1993; US-144992.
06-JUN-1995; US-469537.
(REGE-) REGENERON PHARM INC.
                                                                                                                                                                    Protein tyrosine-kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes nuclear dear the corresponding prot ror-2, ehk-1 and ehk-2. Also described are the corresponding prot Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor tyrosine kinases. The present sequence represents rat Ehk-2. Sequence 948 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat receptor tyrosine kinase Ehk-2.
Receptor tyrosine kinase; Ror-1; Ror-2; Ehk-:
neurotrophin activity; trkB; protto-oncogene;
binding protein; BDNF; NT-3; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Maisonpierre PC, M
WPI; 99-044584/04.
N-PSDB; V70208.
                                                                                                                                                             differentiation.
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The present invention describes nucleic acid
                                                                                                                                                Homo sapiens
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571. .98
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20. .547
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548. .57
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74.0%;
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                                                                                                Sig_peptide
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Intracellular_tyrosine-kinase_domain
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Pred. No. 1.5e-88;
1; Mismatches 24
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Best Local S
Matches 162
                                                                                                                                                                                                         26-OCT-1995.
14-APR-1995; U04681.
15-APR-1994; US-229509.
(AMGE-) AMGEN INC.
(AMGE-) AMGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kinase(s) - also activate chimeric protein tyrosine kinase(s) - also activate chimeric proteins of kinase extracellular domain and Ig constant domain, useful for studying, and therapeutic modulation of, cell growth and differentiation Disclosure; Page 95-99; 125pp; English.

DNA probes based on protein tyrosine-kinase (pTK) sequences were used to screen cDNA libraries to identify novel pTK genes. The bpTKS, bpTK1, bpTK2, bpTK3, bpTK4, bpTK5 and bpTK7 (R85924-28 and R85935, respectively) are expressed in human brain tissue and show homology to known pTKs. A full-length sequence for bpTK7 (R85936) was also obtd. bpTK7 can be used to design drugs that modulate pTK activity. Sequence 986 AA;
Claim 18; Page 62-65; 133pp; English.

4 Novel human EPH-11ke receptor profesin tyrosine kinases, HEK5, HEK7, HEK8 and HEK11 (R85089-92), respectively, were identified following isolation of their encoding cDNAs (T02946-49) from a human foetal brain cDNA library. HEK5, HEK7 and HEK8 show extensive homology to the catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8. HEK11 shows no homology to any known EPH-like receptor. Recombinant HEK receptors (or their soluble extracellular domains) are produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wood
                                                                                                                                                                                                                                                                                                                    EPH-like receptor protein tyrosine kinase HEK8.
EPH-like receptor protein tyrosine kinase; PTK; HEK8;
human eph-like kinase; therapy; diagnosis; vector; antibody.
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Bennett BD, Goedd
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12-OCT-1995.
04-APR-1995; U04228.
04-APR-1994; US-222616.
                                                                                                                                                         New nucleic acid encoding and related vectors, host
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95-366160/47.
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95-373799/48.
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                                                                                                                                                                                                                                                                                                                                                                                                   standard;
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                                                                                                                                        id encoding EPH-like receptor tyrosine kinase(s) ctors, host cells, proteins, antibodies etc., used and therapeutically to modulate receptor activation
                                                                                                                                                                                                                                                                                                                                                                                                 Protein;
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73.3%;
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Best Local S
Matches 162
                                                                                                                                                                                                                                                                                              (ZHOU/) ZHOU N. (ZHOU/) ZHOU N. W. KIOMET LF, Schulz NT, W. WPI; 98-541751/46.
injuries, neurischizophrenia, c
                                                                                                                                                                                                                                                                                                                                                                                                       US5814479-A.
29-SEP-1998.
11-JUN-1996; 673789.
04-JAN-1994; US-177812.
11-JUN-1996; US-673789.
                      Claim 1; Fig 2; 72pp; English.

Claim 1; Fig 2; 72pp; English.

The present sequence represents mouse Bsk, which is a receptor-like tyrosine kinase. The nucleic acid sequence encoding Bsk can be used in Bsk nucleic acid probes, which can be used in detecting alterations in the level of Bsk messenger-RNA (mRNA) in biological samples isolated from a mammal afflicted with a disease, such as neurodegenerative diseases or disorders and neoplasms. The nucleic acid sequence can also be delivered into the limbic system of patients with limbic system neurodegenerative disease, disorder or injury, to promote or enhance limbic system neuron regeneration or growth. Such neurodegenerative diseases include, chromosomal abnormalities, degenerative growth and development disorders, viral infections, bacterial infections, brain injuries, neoplastic conditions, Alzheimer's disease, epilepsy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression cells, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse; Bsk; receptor-like tyrosine kinase; brain; diagnosis; neoplasm; neurodegenerative disease; limbic system neuron regeneration; chromosomal abnormality; degenerative growth; development disorder; viral infection; bacterial infection; Alzheimer's disease; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    therapeutically to receptors.
                                                                                                                                                                                                                   with disease
Claim 1; Fig
                                                                                                                                                                                                                                                              Isolated nucleic acid sequence encoding nucleic acid probes, used in detecting a
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                                                                                                                                                                                                                                                   messenger-RNA in
                                                                                                                                                                                                                                                                                                                                                                            (KROM/) KROMER L F. (SCHU/) SCHULZ N T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse Bsk receptor-like
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ZHOU R.
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Pred. No. 1.4e-87;
0; Mismatches 28;
                    cerebral ischaemia
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Best Local S
Matches 151
                                                                                                                                                                                                                                                                                                                                                                                               Matches
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01-DEC-1998.
06-JUN-1995; 469537.
17-MAR-1995; US-406247.
17-MAR-1995; US-36559.
28-OCT-1993; US-144992.
06-JUN-1995; US-469537.
(REGE-) REGENERON PHARM INC.
MAISORDIETTE PC, MAISAKOWSKI I
WPI, 99-044584/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               proteins
Example; Fig 22; 194pp; English.
The present invention describes nucleic acid molecules for ror-1,
ror-2, ehk-1 and ehk-2. Also described are the corresponding proteins:
Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor
tyrosine kinases. The present sequence represents rat Ehk-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat receptor tyrosine kinase Ehk-1.

Receptor tyrosine kinase; Ror-1; Ror-2; Ehk-1; Ehk-2; detection; neurotrophin activity; trkB; proto-oncogene; tyrosine kinase receptor; binding protein; BDNF; NT-3; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding receptor
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|VNHSVTDDPPKMHCSAEGEWLVPIGKCMCKAGYEEKNGTCQ
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|GLGTCKETFNMYYFESDDENGRSIKENQYIKIDTIAADESFTELDLGDRVMKLNTEVRDV
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Pred. No. 1.7e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                Score 866.5; DB 1;
Pred. No. 2.1e-83;
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The angiogenesis-related conditions.

Example 1; Page 50-53; 75pp; English.

Example 1; Page 50-53; 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 72.1
Best Local Similarity 68.3
Matches 151; Conservative
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09-MAY-1996.
26-OCT-1995; U14016.
27-OCT-1994; US-330128.
07-JUN-1995; US-486449.
(GETH) GENERYECH INC.
R85090 standard; Protein; 991 AA.
R85090;
16-APR-1996 (first entry)
EPH-11ke receptor protein tyrosine kinase HEK7.
EPH-11ke receptor protein tyrosine kinase; PTK;
human eph-11ke kinase; therapy; diagnosis; vector
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GETH ) GENENTECH INC.
Caras IW, Winslow JW;
WPI; 96-239448/24.
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05-JAN-1997 (first entry)
Rat REK7 eph-related tyrosine kinase receptor.
REK7; eph-related tyrosine kinase receptor; AL-1; ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; T18893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV 120
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58. .462
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58. .928
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Best Local S
Matches 150
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14-APR-1995; U04681.
15-APR-1994; US-229509.
(AMGE-) AMGEN INC.
FOX GM, Jing S, Welcher A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or prodn.

Claim 18; Page 54-57; 133pp; English.

4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7

4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7

HEK8 and HEK11 (R85089-92), respectively, were identified following

isolation of their encoding cDNAs (T02946-49) from a human foetal br.

CDNA library. HEK5, HEK7 and HEK8 show extensive homology to the

catalytic domain of chicken EPH-like receptors CeK5, Cek7 and Cek8.

HEK11 shows no homology to any known EPH-like receptor. Recombinant

HEK receptors (or their soluble extracellular domains) are produced i

expression of encoding sequences in procaryotic or eucaryotic host

cells, and are used to produce antibodies (utilised in diagnostic

assays), or to identify and purify ligands for HEK receptors, or

therapeutically to modulate the activation of cell-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid encoding EPH-like receptor tyrosine kinase(s) and related vectors, host cells, proteins, antibodies etc., used diagnostically and therapeutically to modulate receptor activation
                                                                                                                                                                                                              Mouse developmental kinase 1 MDK1 T1.

Mouse developmental kinase 1; MDK1 T1; receptor tyrosine kinase;

MOK1 T1; receptor tyrosine kinase;

MOK1 T1; receptor tyrosine kinase;
   misc_difference
                                                              modified_site
                                                                                           modified_site
                                                                                                                        modified_site
                                                                                                                                                                                                   neurodegeneration; neuroproliferation;
                                                                                                                                                                                                                                                                                            W03422 standard; Protein;
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                                 domain
                                                                                                                                                      peptide
                                                                                                                                                                                   Mus sp.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLGTCKETFNMYYFESDDQNGRNIKENQYIKIDTIAADESFTELDLGDRVMKLNTEVRDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WEEIGEVDENYAPIHTYQVCKVMEQNQNNWLLTSWISNEGASRIFIELKETLRDCNSLPG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WEEISGYDEHYTPIRTYQYCNYMDHSQNNWLRTNWYPRNSAQKIYYELKFTLRDCNSIPL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GM, Jing S,
95-373799/48.
                                                                                                                                                                                                                                                                                                                                                                        VNHSVTDEPPKMHCSAEGEWLVPIGKCMCKAGYEEKNGTCQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                   GPLSKKGFYLAFQDVGACIALVSVRVYYKKCPSVVRHLAVFPDTITGADSSQLLEVSGSC
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                                              410. .41
/label=
                                                                                                                         /label= Sig_peptide 64..66
                                                                                                                                                                    Location/Qualifiers
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                                                                                                        /label- N-glycosylation_site
                 /label=
                                                            el= N-glycosylation_site
.412
                                                                                           . 345
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                              .579
            Transmembrane_domain
                                           N-glycosylation_site
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Matches 156
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03-JAN-1995; US-368776.
03-JAN-1995; US-368776.
(PLAC) MAX PLANCK GES F
(SUGE-) SUGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; page 109-111; 128pp; English.

CDNA cloning using adult mouse brains and Northern blotting identified 2 truncated versions, MDKI T1 (W03422) and MDKI T2 (W03423), of the novel mouse developmental kinase 1 (MDKI) (see als W03423), a new member of the eck/eph family of receptor tyrosine kinases. Their amino acid sequences were deduced from cDNA clones (T32961 and T32962) obtd. from adult mouse brains. MDK T1 and T2 each possess the entire ectodomain, the transmembrane domain and part of the juxtamembrane region of MDKI, but lack the catalytic tyrosine kinase domain. They can be used to screen for potential agents useful for treatment of diseases characterised by abnormal transduction.
                                                                                                                                                                              Mouse developmental kinase 1 MDK1 T2.

Mouse developmental kinase 1; MDK1 T2; receptor tyrosine kinase; RTK; signal transduction; probe; diagnosis; gene therapy; neurodegeneration; neuroproliferation; cancer.
  WO9621013-A1
                         misc_difference
                                                                                              modified_site
                                                                                                                                            peptide
                                                                                                                                                                                                                                                       W03423 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New mouse development kinase 1 gene - use diagnosis and treatment of abnormalities
                                                                      modified_site
                                                                                                                     modified_site
                                                                                                                                                           Key
                                                                                                                                                                    Mus sp.
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555. .57
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                                                                                            /label= N-glycosylation_site 343..345
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                                                                                   /label-
                                                                                                                                /label Sig_peptide
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                                                                     el- N-glycosylation_site
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                                             l= N-glycosylation_site
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            "product
                                    Transmembrane_domain
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Pred. No. 9.2e
36; Mismatches
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            of
            alternative
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           splicing"
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W09621013-A1.
11-JUL-1996.
03-JAN-1995; U00419.
03-JAN-1995; US-368776.
(PLAC ) MAX PLANCK GES I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; page 113-115; 128pp; English.

CDNA cloning using adult mouse brains and Northern blotting
identified 2 truncated versions, MDK1 T1 (W03422) and MDK1 T2
(W03423), of the novel mouse developmental kinase 1 (MDK1) (see also
W03421), a new member of the eck/eph family of receptor tyrosine
kinases. Their amino acid sequences were deduced from cDNA clones
(T32961 and T32962) obtd. from adult mouse brains. MDK T1 and T2
each possess the entire ectodomain, the transmembrane domain and
part of the juxtamembrane region of MDK1, but lack the catalytic
tyrosine kinase domain. They can be used to screen for potential
agents useful for treatment of diseases characterised by abnormal
signal transduction.
                                                                                                                                                                                                        W03421 standard; Protein; 998 AA.
W03421;
11-NOV-1996 (first entry)
Mouse developmental kinase 1.
Mouse developmental kinase 1; MDK1; receptor tyrosine
signal transduction; probe; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-JUL-1996.
03-JAN-1996; U00419.
03-JAN-1995; US-368776.
03-JAN-1995; US-368776.
(PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
(SUGE-) SUGEN INC.
Clossek T, Millauer B, Ullrich A;
WPI; 96-333988/33.
                                                                                                                                                                               Mus sp.
Key
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New mouse development
                                                                                              modified_site
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                                                                                                                                           modified_site
                                                                                                                                                                                                   neurodegeneration; neuroproliferation;
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|::::| |: |||:|| |||||||| | |||:::| |:
VSSAEEEAENSPRMHCSAEGEWLVPIGKCICKAGYQQKGDTCE 277
                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                     /label=
555. .57
                                                                                                                                          /label=
64. .66
                                                          555. .579
/label- Tr
                                                                                            7label= N-glycosylation_site
343 .345
7label= N-glycosylation_site
410 .412
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int of ab
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abnormalities
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Pred. No. 9.5e-83;
 WISSENSCHAFTEN
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ynal transduction
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Best Local Similarity
Matches 156; Conserv
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Clossek T, Millauer B, Ullric
WPI: 96-333988/33.
N-PSDB; T32960.
New mouse development kinase 1
New mouse development kinase 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse developmental kinase 1 (MDRI) (MO3421) is a new member of eck/eph family of receptor tyrosine kinases (RTKs). Its amino acid sequence was deduced from a cDNA clone (T32960) isolated from mouse embryo and adult brain libraries. The distinct patterns of MDRI expression during mouse development suggest an important role for MDRI in the formation of neuronal structures. MDRI may be obtd. by expression in host cells. It can be used in methods for the diagnosis of diseases characterised by abnormality in a signal transduction pathway, such as neuroproliferative or neurodegenerative disorders or cancer, to screen for (ant)agonists, and to raise antibodies. Sequence 998 AA;
               Claim 18; Page 71-75; 133pp; English.

4 Novel human EPH-11ke receptor protein tyrosine kinases, HEK5, HEK7, HEK8 and HEK11 (R85089-92), respectively, were identified following isolation of their encoding cDNAs (T02946-49) from a human foetal brain cDNA library. HEK7 and HEK8 show extensive homology to the catalytic domain of chicken EPH-11ke receptors Cek5, Cek7 and Cek8. HEK11 shows no homology to any known EPH-11ke receptor. Recombinant HEK receptors (or their soluble extracellular domains) are produced by
                                                                                                                                                              New nucleic acid encoding EPH-like receptor tyrosine kinase(s) and related vectors, host cells, proteins, antibodies etc., us diagnostically and therapeutically to modulate receptor activa
                                                                                                                                                                                                                                                                                                                             Homo sapiens.
WO9528484-A1.
                                                                                                                                                                                                                                                                                                                                                      EPH-like receptor protein tyrosine kinase HEK11.
EPH-like receptor protein tyrosine kinase; PTK; HEK11;
human eph-like kinase; therapy; diagnosis; antibody; vector.
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                                                                                                                                                                                                                               Fox GM, Jing S, WPI; 95-373799/48.
                                                                                                                                                                                                                                       (AMGE-) AMGEN INC.
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15-APR-1994; US-229509
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6; Mismatches 28;
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07-SEP-1994; U10140.
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(LJOL-) LA JOLLA CANCER R
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Probes derived from the EPH-related PTKS Cek4 (090659) and (090660) were used to isolate novel cDNA clones (090652-58, 090661-62) from chicken embryo and embryonic brain librarie Sequence 995 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R75712 standard; Protein;
R75712;
11-NOV-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cells, and are used to produce antibodies (utilised in diagnostic assays), or to identify and purify ligands for HEK receptors, or therapeutically to modulate the activation of cell-associated receptors.

Sequence 998 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pasquale EB, Sajj. WPI; 95-215256/28.
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08-JUN-1995; U10140.
07-SEP-1994; U5-162809.
03-DEC-1993; U5-162809.
(LJOL-) LA JOLLA CANCER RE.
Pasquale EB, Sajjadi FG;
WPI; 95-215256/28.
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R75709;
11-NOV-1995
                                                                                                                                                                                                                                         Claim 11; Page 71-75; 129pp; English.

A cDNA clone encoding a novel variant of EPH-related PTK Cek5+ (290657), was isolated from a chick embryo library lambda gtl1. Cek5+ protein (R75709) contains a 16-amino insertion in the juxtamembrane domain, and be a result of alternative splicing. Cek5+ is exclusively expressed in sequence 1011 AA;
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RGTCISNAEEVDVPIKLYCNGDGEWLVPIGRCMCRPGYESVENGTVCR
                                            IREVGEVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEV
                                                                                         VPGSCKETFNLYYYESDFDSATKTFPNWMENPWMKVDTIAADESFSQVDLGGRVMKINTE
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Q91694 xenopus lae
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Q42422 gallus gall
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Q15197 homo sapien
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Q3xtj2 bacteriopha
Q61066 craterostig
Q33642 salmonella
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-!- -!- -!- EMBL HSSP PROS	: : : : : : : : : : : : : : : : : : :	Mech		GN PAG. GN Yenopus OC Eukaryot OC Batrachi OC Xenopus		169 102
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SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2 SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-L. SIMILARITY: TO OTHER PROTEIN TYROSINE KINASES DOMAIN. BELONGS TO THE EPH FAMILY. ; L25099; AAA64464.1; ; P00523; 2PTK. ; P00523; 2PTK. ; P800107; PROTEIN_KINASE_ATP; 1. itte; PS00109; PROTEIN_KINASE_TYR; 1.	SUBCLIFICATION: TYPE I MEMBRANE PROTEIN. TISSUE SPECIFICITY: LOCALIZED EXPRESSION IN A CREST AND NEURAL TISSUES IN EMBRYOS. DEVELOPMENTAL STAGE: PRESENT TRANSIENTLY IN VI EXPRESSED IN THE FOREBRAIN, RHOMBOMERES R3 AND AND IN THE PROMEPHYON	TISSUES IN XENOPUS LAEVIS EMDIYOS."; MECH. Dev. 46:219-229(1994). -!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN SIMILARITY). MAY PLAY A ROLE IN THE DIFFEREN NEURAL CREST AND OTHER TISSUES. -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE TYROSINE PHOSPHATE.	[1] [1] TISSUDENEE FROM N.A. TISSUDENBURAL CREST; MEDLINE; 95001564. MYLNNING R.S., SARGENT T.D.; "Pagliaccio, a member of the Eph family of genes, has localized expression in a subset	(PAGLIACCIO). PAG. Xenopus laevis (African clawed frog). Xenopus laevis (African clawed frog). Butrachia; Anura; Mesobatrachia; Pipoid Xenopus.	01, 01, 12, RECE	PRELIMINARY;
IMMUNOGLOBULIN-L FIBRONECTIN TYPE ROTEIN TYPOSINE K. EPH FAMILY	PE I MEMBRA LIZED EXPRE IN EMBRYOS SENT TRANSI	bryos."; EMBERS OF T ROLE IN THE ISSUES. A PROTEIN	Eph family	ed frog). ; Craniata; hia; Pipoid	01, Created) 01, Last sequen 12, Last annota RECEPTOR PAG PR	PRT; 985
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS. SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPH FAMILY. (126099; BAA64464.1; (126099; BAA64464.1; (126) P00523; 2PTK. (136) PROTEIN_KINASE_ATP; 1. (137) PROTEIN_KINASE_TYR; 1.	SUBCLIFIED TO THE I MEMBRANE PROTEIN. TISSUE SPECIFICITY: LOCALIZED EXPRESSION IN A SUBSET OF NEURAL CREST AND NEURAL TISSUES IN EMBRYOS. DEVELOPMENTAL STAGE: PRESENT TRANSIENTLY IN VISCERAL ARCH 3. ALSO EXPRESSED IN THE FOREBRAIN, RHOMBOMERES R3 AND R5 OF THE HINDBRAIN AND IN THE PROMEDEROS.	US laevis embryos."; 9-229(1994). CEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY (BY MAY PLAY A ROLE IN THE DIFFERENTIATION OF CRANIAL AND OTHER TISSUES. TIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN SCHATE.	[1] [1] [1] [1] [1] [1] [1] [1] [1] [1]	0). svis (African clawed frog). Metazoa; Chordata; Craniata; Vertebrata; Amphibia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae;	ted) sequence update) annotation update) PAG PRECURSOR (BC 2.7.1.112)	5 AA.

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Q1-NOV-1996 (Tremblrel. 0
Q1-NOV-1999 (Tremblrel. 1
TYROSINE-PROTEIN KINASE R
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MEDLINE; 96125143.
XU Q., ALLDUS G., HOLDER N
"Expression of truncated 5
segmental restriction of c
hindbrain.";
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PRINTS; PRO0014; FNTYPEIII.
Transferase; Tyrosine-protein
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                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
Batrachia;
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| ||||:::||||||: | |
31 VTLLDSRSVQGELGWIASPLEG
               DEVELOPMENTAL STAGE: EXPRESSION OCCURS IN 73, R5 AND TRANS:
AT LOWER LEVELS IN R2.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: TO OTHER PROTEIN-TYPOSINE KINASES IN THE CATALL
DOMAIN. BELONGS TO THE EPH FAMILY.
                                                                                                     SUBCELLULAR LOCATION: TYPE I MEMBRANE I DEVELOPMENTAL STAGE: EXPRESSION OCCURS
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PF00069;
PF00536;
PF01404;
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Anura; Mesobatrachia; Pipoidea;
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; SAM; 1.
; EPH_lbd; 1.
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RECEPTOR SEK-1 PRECURSOR (E
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Sek-1 receptor tyrosine kinase disrupts the
gene expression in the Xenopus and zebrafish
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CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN (BY S
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FIBRONECTIN TYPE-III (BY SIM
FIBRONECTIN TYPE-III (BY SIM
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PHOSPHORYLATION (AUTO-) (
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Pred.
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ia; Pipoidea; Pipidae;
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PPH-LIKE KIMASE 1 PRECURSOR (F
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SEQUENCE
                                                                                                           BOVENKAMP D.E., GREER P.;
BOVENKAMP D.E., GREER P.;
"Novel Eph-family receptor tyrosine kinase is widely expressed in the "Novel Eph-family receptor tyrosine kinase is widely expressed in the developing zebrafish nervous system.";
Dev. Dyn. 209:166-181(1997).
-i- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY. MAY PLAY A ROLE IN EARLY PATTERN FORMATION WITHIN THE DEVELOPING NERVOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; POO
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PFAM; PF00069; pkinase; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF01404; EPH_Lbd; 1.
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                  Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neopterygii; Teleostei; Euteleostei; Ostariophysi; (
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
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                                                                    SYSTEM.
CATALYTIC ACTIVITY:
TYROSINE PHOSPHATE.
                                 SUBCELLULAR LOCATION:
TISSUE SPECIFICITY: WJ
                     NERVOUS
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PS00109; PROTEIN_KINASE_TYR; 1.
PS00790; RECEPTOR_TYR_KIN_V_1;
PS00791; RECEPTOR_TYR_KIN_V_2;
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PROTEIN-TYROSINE KINASES
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Pred. No. 0.00
4; Mismatches
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ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL). IG-LIKE C2-TYPE DOMAIN (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYROSINE-PROTEIN EXTRACELLULAR (PC POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (BY SIMIL)
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION (AUTO-) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                     I MEMBRANE
EXPRESSED 1
                                                                                           PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               981 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal;
                                                                                             TYROSINE -
                                   E PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .00037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 986
                                     DEVELOPING ZEBRAFISH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BY
(BY
 IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                             Agg
                                                                                                                                                                                                                                                                                                                     cypriniformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
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                                                                                             PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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RESULT
042422
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Best Local Similarity
Matches 13; Conser
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R HSSP; P00523; 2PTK.

R ZIN; ZDB-GENE-990K15-58; Zekl.

R PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

R PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; FALSE_NEG.

PPAM; PF00069; Pkinase; 1.

R PPAM; PF00140; EPH_Lbd; 1.

R PPAM; PF00140; EPH_Lbd; 1.

R PPAM; PF00041; fn3; 2.
                                                                                                                                                                                                    042422 PRELIMINANA,
042422;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-JAN-1998 (TREMBLrel. 12, Last annotation updat
EPH-LIKE RECEPTOR TYROSINE KINASE PRECURSOR (EC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DOMAIN
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DISULFID
BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
VARIANT
SEQUENCE
    ARAUJO M., NIETO M.A.;
"The expression of chick EphA7 during segmentation peripheral nervous system.";
Mech. Dev. 68:173-177(1997).
-!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN FA-!- CATALYTIC ACTIVITY: ATP + A DROTTEN TYPOGETYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
                                                                                              TISSUE-EMBRYO;
MEDLINE; 98092111.
                                                                                                                                SEQUENCE FROM
                                                                                                                                                                           Eukaryota;
                                                                                                                                                                                          Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase;
                                                                                                                                                           Neognathae; Galliformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                 30
                                                                                                                                                                                                                                                                                                                                                                                                                   1 VNLLDSKTIQGELGWISYPSHG
                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                                VTLLDSMSAPGDLGWEAYPSEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transmembrane;
                                                                                                                                                                           Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326
439
626
632
71
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tyrosine-protein kinase; ATP-binding; Phosphorylation; ansmembrane; Glycoprotein; Signal; Immunoglobulin domain.
                                                                                                                              N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata;
rmes; Phasianidae; Phasianinae; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        109654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.7%;
59.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein;
BY SIMILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN KINASE.
AIP (BY SIMILARITY).
BY SIMILARITY.
AIP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ů.
                                                                                                                                                                                                                                                                                                                                                                                                51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 71;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
POTENTIAL.
POTENTIAL.
S -> N.
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CYS-RICH.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPH-LIKE KINASE 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10D38182 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13;
0.0067;
                                                                                                                                                                                                                                    update)
(EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 981;
    FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                0f
                                                                                                                                                           ; Archosauria; Aves; Gallus.
    ADP + PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY)
                                                                the
                                                                central
                                                                                                                                                                                                                                      (TYROSINE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>,,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
RESULT CONTROL OF CONT
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Query Match
Best Local S
Matches 14
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PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PFAM; PF00041; fn3; 2.
PFAM; PF00059; PKINASE; 1.
PFAM; PF00595; SAM; 1.
PFAM; PF01404; EPH_Lbd; 1.
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                            NP_BIND
DISULFID
BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
DOMAIN
TRANSMEM
SEQUENCE MEDLINE;
                                                         Eukaryota;
Batrachia;
                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1999 (TrEMBLrel. 12, EPHRIN TYPE-B RECEPTOR XEK I
                                                                                                                                                                                         Q91571
Q91571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
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DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor;
SIGNAL
                                                      Xenopus laevis (African clawed frog)
Eukaryota; Metazoa; Chordata; Crania
Batrachia; Anura; Mesobatrachia; Pip
                                                                                                       XEK
                                         Xenopus
                                                                                                                   KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0014; FNTYPEIII
                                                                                                                                                                                                                                                                                                                                     Local Similarity 63. nes 14; Conservative
                                                                                                                                                                                                                                                                              ^{3}
                                                                                                                                                                                                                                                                                               1 VNLLDSKTIQGELGWISYPSHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: WITHIN THE NERVOUS SYSTEM, EXPRESSION IS
RESTRICTED TO PROSONERES I AND 2 IN THE DIENCEPHALON AND ALL THE
RHOMBOMERES IN THE HINDBRAIN DURING SEGMENTATION STAGES, LATER ON,
A SUPERIMPOSED PATTERN APPEARS THAT CORRELATES WITH THE FORMATION
OF SEVERAL AXONAL TRACTS. IN THE SOMITIC MESODERM, THE EXPRESSION
CORRELATES WITH SEGMENTATION AND THE GUIDANCE OF BOTH NEURAL CREST
AND MOTOR AXONS THROUGH THE SCLEROTOMES.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
POWART OF THE PROTEIN TRACTS IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                     G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYROSINE PHOSPHATE
                                                                                                                                                                                                                                                                              VILLDSKAQQTELEWISSPPNG
                                                                                                                 RECEPTOR
 95215070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                               993
                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tyrosine-protein kinase; ATP-binding; Phosphorylation; ansmembrane; Glycoprotein; Signal; Immunoglobulin domai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAA74643.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                 XEK).
                                                                                                                                                                                                                                                                                                                                                                                                                             993
551
572
993
116
328
438
642
109
642
753
785
343
                                                                                                                                                                                                                                                                                                                                                     51.3%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                               111366
                                                                                                                                                                                                                                                                                                                                                    . 68;
                                                                                                                            , Last sequence update)
, Last annotation update)
PRECURSOR (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                               WW;
                                                                                                                                                                                                                                                                                                        22
                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                              54
                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
FIBROTEIN KINASE.
PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL). IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYS-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PHOSPHORYLATION (AUTO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPH-LIKE RECEPTOR TYROSINE KINASE. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                       Craniata;
                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                        Pipoidea;
                                                                                                                                                                                                                                                                                                                                                     NO.
                                                                                                                                                                                                        985
                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                           DB .
1.26;
                                                                       Vertebrata;
                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                   13;
                                                        Pipidae;
                                                                                                                                                                                                                                                                                                                                                                 Length 993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY
                                                                                                                                                                                                                                                                                                                                      Indels
                                                      Xenopodinae;
                                                                       Amphibia;
                                                                                                                              (TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain.
                                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT 6
Q91735
ID Q91735
AC Q91735;
DT 01-NOV-1996 (
DT 01-NOV-1996 (
DE EPHRIN TYPE-B
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                                                                                                                                                                                                                Matches
                                                                                                                                                                    Query Match
Best Local
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DISULFID
BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00343; GRAM_POS_ANCHORING; UN PROSITE; PS00107; PROTEIN_KINASE_ATP; 1. PROSITE; PS00109; PROTEIN_KINASE_TYR, IN PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -I- DEVELOPMENTAL STAGE: MATERNALLY EXPRESSED, IT DECREASES AT MID BLASTULA TRANSITION AND REAPPEARS AT LATE NEUTULATION. EXPRESSED AT HIGHER LEVELS IN THE ANTERIOR AND DORSAL REGIONS OF EMBRYONIC STAGES 16, 24 AND 37. IN ADULT IT APPEARS TO BE UBIQUITOUSLY EXPRESSED WITH HIGHER EXPRESSION IN BRAIN AND OVARY. EXPRESSION THE BRAIN, BRACHIAL ARCHES, TRIGEMINAL FACIAL GANGLION, AND THE RETINA OF SWIMMING TADPOLE STAGE OF DEVELOPMENT.
-I- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FRAILY.
-I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
-I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
-EMBL. 1014164; AAA74888.1; -.
                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00041; fn3; 2.
PFAM; PF00069; pkinase; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF01404; EPH_lbd; 1.
                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                               Transterase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00109; TYRKINASE.
                                                                                                                 24
                                                                                                                                   3 LLDSKTIQGELGWISYPSHG
                                                                                                                 LMDTRTATAELGWTANPSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P00523; 2PTK.
                                                                                                                                                           l Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane;
(TremBLrel. 01, Created)
(TremBLrel. 01, Last sequence update)
(TremBLrel. 12, Last annotation update)
-B RECEPTOR PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
                                                                                                                                                           Conservative
                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Tyrosine-protein
                                                                                                                                                                                                                                     48.7%;
50.0%;
                                                                                                                                                                                                               110104
                                                                                                                                                                                                                                                                                                                                                                                                                        otein kinase; ATP-binding; Phosphorylation;
Glycoprotein; Signal; Immunoglobulin domain.
POTENTIAL.
                                                                                                                 43
                                                                                                                                    22
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                                                                                                                                                                                                                                                                  PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY.
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                          4
                                                                                                                                                        Score 58; DB 13;
Pred. No. 0.76;
4; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                             EPHRIN TYPE-B RECEPTOR XEK POLY-LEU.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                       FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL). IG-LIKE C2-TYPE DOMAIN. CYS-RICH.
                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                   PHOSPHORYLATION (AUTO-) (POTENTIAL).
POTENTIAL.
POTENTIAL.
                                                         PRT;
                                                         974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FALSE_NEG
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                                                                                                                                                                                                                                                                                                                                                                                                              RECEPTOR XEK.
                                                                                                                                                        6,
                                                                                                                                                                             Length 985;
                                                                                                                                                        Indels
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RESULT
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ID 04
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Best Local S
Matches 9
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HSSP; P00523; 2PTK.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PFAM; PF00041; fn3; 2.

PFAM; PF00536; SAM; 1.

PFAM; PF00536; SAM; 1.

PFAM; PF01404; EPH_lbd; 1.
043477;
                                                                                                                                                   CARBOHYD
SEQUENCE
                                                                                                                                                                    ACT_SITE
MOD_RES
CARBOHYD
                                                                                                                                                                                                             NP_BIND
DISULFID
                                                                                                                                                                                                                                                                                 TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                     CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                        Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCALES J.B., WINNING R.S., RENAUD C
"Novel members of the eph receptor
during Xenopus development.";
Oncogene 11:1745-1752(1995).
-i- FUNCTION: RECEPTOR FOR MEMBERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00109; TYRKINASE.
PRINTS; PR00014; FNTYPEIII.
Transferase; Tyrosine-protein
                                                                                                                                                                                                    BINDING
                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: TYPE I M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -I- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE --
TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus.
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                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                            DOMAIN
                                                           21 LMDTKWTTSELAWVAYPDSG
                                                                             3 LLDSKTIQGELGWISYPSHG
                               7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY).
                                                                                                  Similarity 45.
9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96068901.
                                                                                                                                                                                                                                                                                                                                  Transmembrane;
                                                                                                                                                   974 AA;
                                                                                                                                                                                                             535
556
531
178
316
424
609
609
           PRELIMINARY;
                                                                                                          47.9%;
                                                                                                                                                   108263
                                                                                                                                                                                                                                                                                                                       otein kinase; ATP-binding; Phosphorylation;
Glycoprotein; Signal; Immunoglobulin domai
POTENTIAL.
                                                           40
                                                                              22
                                                                                                                                                   WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RENAUD C
                                                                                                4;
                                                                                                Score 57; DB Pred. No. 1.1; 4; Mismatches
                                                                                                                                                                    PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY.
ATP (BY SIMILARITY).
BY SIMILARITY.
ENOSPHORYLATION (AUTO-) (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                      CYTOPLASMIC (POTENTIAL) IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                         FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                              CYS-RICH
                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                             EPHRIN TYPE-B RECEPTOR
          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I MEMBRANE PROTEIN
SED IN THE EMBRYO I
                                                                                                                                                   BD419F6D CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.S., SHEA L.J.,
tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF THE
          1055 AA
                                                                                                                    DB 13; Length 974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPHRIN-B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IN PRE-SOMITIC
                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OVARY. LOWER LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAMILY
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subfamily exp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xenopodinae;
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Best Local S
Matches 10
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HSSP; P00523; 2PTK.
HSSP; P00523; 2PTK.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PFAM; PF01404; EPH_lbd; 1.
PFAM; PF004041; fn3; 2.
PFAM; PF00069; Pkinase; 1.
PFAM; PF00069; Pkinase; 1.
PFAM; PF00536; SAM; 1.
                                                                                                                                                                                                                                                                                                    STEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998 (TrembLrel. 06, Created)
01-JUN-1998 (TrembLrel. 06, Last sequence up
01-NOV-1999 (TrembLrel. 12, Last annotation
EPH-LIKE RECEPTOR TYROSINE KINASE HEPHB1C
(EPH-LIKE RECEPTOR TYROSINE KINASE HEPHB1D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             043569
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TANG X.X., PLEASURE D.E., IN
Submitted (SEP-1997) to the
EMBL; AF025304; AAB94602.1;
HSSP; P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998
01-JUN-1998
                                                                                                                                                       EMBL;
EMBL;
HSSP;
PFAM;
                                 PFAM; P
PRINTS;
                                                                                                                                                                                                                                                                            STEIN E.,
Submitted
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PRINTS; PRO0109; TYRKINASE.
TYROSINe-protein kinase.
SEQUENCE 1055 AA; 117492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                   TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                             Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN-TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23
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N E., SCHOECKLMANN H.O., D

11tted (DEC-1997) to the EM-

11ttdd (DEC-1997) to the EM-

11ttd (DEC-1997) to the EM-

11ttd (DE
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                                                                                                                                                                                                                                                                                                                                                                                                                             Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Ve Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.18;
50.08;
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. 06, Last sequence upo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 56; DB Pred. No. 1.7; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MW;
                                                                                                                                                                                                                                                                      EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                       DANIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                       T.O.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vertebrata;
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Matches
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to c-Jun Kinase.";
J. Biol. Chem. 0:0-0(1997).
EMBL; AR037331; AAD02030.1; -
HSSP; P00523; 2PTK.
PROSITE; PS00107; PROTEIN_KIN
PROSITE; PS00109; PROTEIN_KIN
                                                                                                                                                       Q07494
Q07494;
Q1-NOV-1996
Q1-NOV-1999
Q1-NOV-1999
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01-MAY-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  095142;
     expressed.";
Oncogene 8:1807-1813(1993).
EMBL; Z19110; CAA79526.1; -
HSSP; P00523; 2PTK.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS00109; PROTEIN_KINASE_TYR;
                                                                                                            Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                    iPH-La...
EPHB1.
Homo sapiens (Human).
Homo sapiens (Chuman).
'~~vota; Metazoa; Chordata; Cr
'~~vota; Metazoa; Catarrhini;
                                                                                                                                                                                                                                                                                                                 Receptor; Kinase.
SEQUENCE 984 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                  TISSUE-BRAIN;
MEDLINE; 93288594.
SAJJADI F.G., PASC
                                                                                                                                                                                                                                                                                                                                                                                              STEIN E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPH-LIKE
                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                            Five novel
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LMDTRTATAELGWTANPASG
                                                                                                                                                PROTEIN
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                                                                                                                                                                                                                                                                      similarity
9; Conserv
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9 (TrEMBLrel. 10,
9 (TrEMBLrel. 12,
ECEPTOR TYROSINE K
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                                                                                                                                               5 (TrEMBLrel. (5 (TrEMBLrel. (9) (TrEMBLrel. 1) (TrEMBLrel. 1)
                                                         ., PASQUALE E.B.; avian Eph-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                      Conservative
                                                                                            N.A.
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                                                                                                                                                                                                                                                                                                                                PROTEIN_KINASE_ATP;
PROTEIN_KINASE_TYR;
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Last sequence update)
Last annotation updat
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د
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55; DB Pred. No. 2.1; 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata;
                                                                                                                                                                                          PRT;
                                                           tyrosine kinases
                                                                                                                                                                                                                                                                                                                                                                                   CERRETTI D.P., r, EphB1/ELK, co
                                                                                                                                                                                                                                                                                                                 DF5C8ED3
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                                                                                                                                                                                                                                                                                                                                                                                                                               Hominidae;
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                                                                                                                                                                                                                                                                                                                 CRC32;
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on update)
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                                                           differentially
                                                                                                             Archosauria;
Gallus.
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Best Local S
Matches S
                                                                                                                            MIM; 602757; -...

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; FA
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; FA
PRAM; PF00041; fn3; 2.

PFAM; PF00069; Pkinase; 1.

PFAM; PF000536; SAM; 1.

PFAM; PF01404; EPH_1bd; 1.

PFAM; PF01404; EPH_1bd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1998
01-JAN-1998
01-NOV-1999
DOMAIN
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DOMAIN
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                                                              DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE; 97350806.
MATSUCKA H., IWATA N., ITO M., SHIMOYAMA M., NAGATA
TAKAI S., MATSUI T.;
"Expression of a kinase-defective Eph-like receptor
human brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPHBG.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Eukaryota; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           015197
015197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM;
PFAM;
PFAM;
                                                                                                                                                                                                               DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.

-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

EMBL; D83492; BAA21560.1; -.

EMBL; AF107256; AAD03058.1; -.

HSSP; P00523; 2PTK.
                                                                                                                                                                                                                                                                            -1: SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-1: TISSUE SPECIFICITY: STRONG EXPRESSION IN THE BRAIN AND PANCREAS AND WEAK EXPRESSION IN OTHER TISSUES, SUCH AS THE HEART, PLACEN LUNG, LIVER, SKELETAL MUSCLE AND KIDNEY.
-1: SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                               SIGNAL
                                                                                                               PRINTS; PRO0014; FNTYPEIII.
Transferase; ATP-binding; Phosphorylation; Receptor; Transmembrane;
                                                                                                                                                                                                                                                                                                                                                       Submitted (NOV-1998)
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-804 FROM
                                                                                                                                                                                                                                                                                                                                                                                                   Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPH-FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11
                                                                                                                                                                                                                                                                                                                                              FUNCTION: KINASE-DEFECTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LMDTRTATAELGWTANPPSG
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PF01404;
PF00041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 (TrEMBLrel. 05, 098 (TrEMBLrel. 05, 199 (TrEMBLrel. 12, 199 (TrEMBLrel. 12, 199 )
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                                                                                    ; Signal;
1 16
17 1006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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EPH_1bd;
fn3; 2.
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1006
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                                                                                                         Immunog.
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                               OGIODUIN domain.
BY SIMILARITY.
BY SIMILARITY.
EPH-FAMILY RECEPTOR PROTEIN.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
**C-**TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22
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Last annotation update)
PRECURSOR (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ databa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                   IG-LIKE C. POLY-SER. CYS-RICH.
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Pred.
FIBRONECTIN POLY-GLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                             I MEMBRANE PROTEIN.

EXPRESSION IN THE BRAIN AND PANCREAS.
                                                                                                                                                                                                                                                                                                                                                                                                 235:487-492(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D939D7D0 CRC32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vertebrata; Mammalia,
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          TYPE-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAGATA A.,
                                                                                                                                                                                                                                                                                                                                            databases.
EMBERS OF T
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RESULT
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Best Local S
Matches
                                                                                                              MGD; MGI:108444; Cekl.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; FJ
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; FJ
PFAM; PF00041; fn3; 2.

PFAM; PF00069; pkinase; 1.

PFAM; PF00104; EPH_1bd; 1.

PRINTS; PR00014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-BALB/C X 129 F2; TI
MEDLINE; 96358627.
GURNIAK C.B., BERG L.J.;
"A new member of the Eph f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
DOMAIN
DOMAIN
NP_BIND
DISULFID
CARBOHYD
SEQUENCE
 CHAIN
DOMAIN
TRANSMEM
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DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     008644;
                                                                                  Transferase; ATP-binding; Phosphorylation; Re Glycoprotein; Signal; Immunoglobulin domain; SIGNAL 1 32 BY SIMILARTTY
                                                                                                                                                                                                           EMBRYONIC STEM CELLS.

1. SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATA:
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.

1. SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN

1. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

EMBL; L77867; AAB51430.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).

Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-UU-1997 (TrEMBLrel. 04, Created)
01-UU-1997 (TrEMBLrel. 04, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
EPH/ELK RECEPTOR-LIKE PROTEIN PRECURSOR (MEP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1997 (TrEMBLrel.
01-JUL-1997 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                    tyrosine kinase activity.
Oncogene 13:777-786(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CEKL OR MEP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  008644
                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 LLDSKTIQGELGWISYPSHG
                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: HIGH LEVEL IN THYMUS, AND LEVELS OF EXPRESSION IN KIDNEY, LUNG, LIVER, B MUSCLE, SPLEEN FROM 2 WEEK OLD AND ADULT MICE,
                                                                                                                                                                                                                                                                                                       ISOFORMS ARE SECRETED.
ALTERNATIVE PRODUCTS: AT LEAST
ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                  FAMILY
                                                                                                                                                                                                                                                                                                                                                          FUNCTION: KINASE-DEFECTIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLDTTGETSEIGWLTYPPGG
                                                                                                                                                                                                    P00523;
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655
866
661
465
1006
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                                                                                                                                                                                                     2PTK
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1014
591
612
1014
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361
476
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                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-THYMUS;
                                                                                                                                                                                                                                                                                                                                                                              family .";
                                                                                                                                                                                                                                                                                                                                     TYPE I MEMBRANE
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PROTEIN KINASE-LIKE.
POLY-PRO.
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.
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Pred.
                              EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
CYS-RICH.
FIBRONECTIN TYPE-III.
                      POLY-SER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                        EPH/ELK RECEPTOR-LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata;
chi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                           RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                         of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                         receptors
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No.
                                                                                                                                                                                                                                                                                                                 THREE
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5.8;
                                                                                                                                                                   FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                        FOR
                                                                                                                                                                                                                                                                                                                 ISOFORMS
                                                                                                                                                                                                                                                                                                                                     PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
                                                                                           Receptor; Tran
n; Alternative
                                                                                                                                                                                                                                                                                                                                                          MEMBERS
                                                                                                                                                                                                                                                                                                                                                                                        that lacks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1006;
                                                                                                                                                                                                                                                                       D BRAIN. VERY LOW
BONE MARROW, SKI
E, HEART, TESTES
                                                                                                                                                                                                                                                     IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                 ARE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia;
                                                                                                       Transmembrane;
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DOMAIN
                                                                                                                                                           Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacterida; Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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                                                                                                                                                                                                                                                                HYPOTHETICAL
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Actinomycetales; Coryo
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                                                                    HAMLIN N.,
                                                                                           SEQUENCE FROM N.A. STRAIN-H37RV;
                                             Submitted (FEB-1998)
SEQUENCE FROM N.A.
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P -> S (IN CDNA 3).
MISSING (IN CDNA 3).
AIP (BY SIMILARITY).
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P -> PCPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6C314913 CRC32;
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                                      MANTHEWS P.;
Submitted (DEC-1995) to the Enul, Submitted (DEC-1995) to the Enul, EMBL; 269662; CAA93506.1; -.
EMBL; 268214; CAA93506.1; JOINED.
EMBL; 268214; CAA92448.1; -.
EMBL; 269662; CAA92448.1; JOINED.
EMBL; 269662; CAA92448.1; JOINED.
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Best Local Similarity
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Best Local
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Q17901; Q20887;
01-NOV-1996 (TIEMBLICEL: 0:
01-NOV-1998 (TIEMBLICEL: 0:
01-JAN-1999 (TIEMBLICEL: 0:
                                                                                                                                                                                          WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTINGRE B., O'CALLAGHAN M.,
PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN I.
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"MATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COLE S.T., PARKHILL J., Submitted (FEB-1997) to [3]
                                                                                                                         MATTHEWS
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 94150718. WILSON R., AINSCOUGH
                                                                                                                                                                                                                                                                                                                                                                                                                                               C10C5.6A PROTEIN.
C10C5.6A.
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Hypothetical protein.
SEQUENCE 368 AA; 3
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PHILIPP W.J., POULET
BALASUBRAMANIAN V., F
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. MATTHEWS P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. EMBL; AL022004; CAA17617.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COLE S.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-H37RV;
                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-H37RV;
                                                                                                                                                          Nature
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                                                                                                                                                                                                                                                                                                                                                                                                           Rhabditina;
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9; Conservative
                                                                                                                                   FROM N.A.
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; Rhabditoidea;
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B., BERGH
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                                                                                                           the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genome os H37RV,
                                                                                                                                                                                                                                                                                                                                                                                                         oda; Secernentea; Rhabditia;
Rhabditidae; Peloderinae; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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Pred. No. 6.5;
2; Mismatches
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  Score
Pred.
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            DR HSSP; P00523; 2PTK.

NR HSSP; P00523; 2PTK.

NR PRINTS; PR00104; FNTYPEIII.

NR PRINTS; PR00109; TYRKINASE_ATP; 1.

NR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

NR PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

NR PROSITE; PS0011; PRCOTEIN_KINASE_DOM; 1.

NR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

NR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

NR PROSITE; PS00186; EGF_2; UNKNOWN_1.

NR PROSITE; PS00186; EGF_2; UNKNOWN_1.

NR PFAM; PF00041; fn3; 2.

NR PFAM; PF00069; pkinase; 1.

NR PFAM; PF00536; SAM; 1.

NR PFAM; PF00536; SAM; 1.

NR PFAM; PF00536; STAM; 1.

NR PFAM; PF01404; EPH_Lbd; 1.

NR PFAM; PF01505; Tyrosine-protein kinase; ATP-binding; Phosphorylation; KW Receptor; Transmembrane; Glycoprotein; Signal.
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Minimum Maximum

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ALIGNMENTS

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8666.1;		or send an email to license@isb-sib.ch).	requires a license agreement (See http://w	ified and this statement is not removed us	by non-profit institutions as long as its of	the European Bioinformatics Institute There are no restrictions on its	between the Swiss Institute of Bioinformatics and the EMBL outstation -	This SWISS-PROT entry is copyright. It is produced through a collaboration		-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.		-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC	-i- TISSUE SPECIFICITY: GREATEST LEVELS OF EXPRESSION OCCURRING IN THE BRAIN.	-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.		-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +	EPHRIN-A2, -A3, -A4 AND -A5.		New Biol. 3:769-778(1991).	at least two forms of the socostor	from mouse and chicken that is developmentally regulated and encodes	tor tyrosine kinase	Saiiadi F.G., Pasquale E.B., Subramani S.:	MEDLINE; 92031278.	SEQUENCE FROM N.A.	(E)	Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;			XINASE RECEPTOR ETX1) (CEK4).	A RECEPTO	01-NOV-1997 (Rel. 35, Last annotation update)	(hol of tost somes	01-DEC-1992 (Rel 24 Created)		ID EPAS CHICK STANDARD: PRT: 983 AA.	COTTON	1	

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RESULT
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TRANSMEM
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                     Boyd A.W., Ward L.D., Wicks I.P., Simpson R.J., Salvaris E., Wilk Welch K., Loudovaris M., Rockman S., Busmanis I.; "Isolation and characterization of a novel receptor-type protein tyrosine kinase (hek) from a human pre-B cell line."; J. Biol. Chem. 267:3262-3267(1992).
-!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS EPHRIN-A2, -A3, -A4 AND -A5. COULD PLAY A ROLE IN LYMPHOID
                                                                                                                                                                                                                                                                Wicks I.P., Wilkinson D., Salvaris E., Boyd A.W.; "Molecular cloning of HEK, the gene encoding a receptor kinase expressed by human lymphoid tumor cell lines."; Proc. Natl. Acad. Sci. U.S.A. 89:1611-1615(1992).
                                                                                                                                                                                                                                                                                                                                                                                                      EPA3_HUMAN STANDARD; PRT; 9
P29320;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC
KINASE RECEPTOR ETK.) (HEK).
                                                                                                                                FUNCTION.
-I- CATALYTIC ACTIVITY: ATP + A PROTEIN
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Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                          SEQUENCE OF 21-29 AND MEDLINE; 92147681.
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                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
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                                                        PROTEIN TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: RESTRICTED TO LYMPHOID TUMOR CELL LIN
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATA
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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EPHRIN TYPE-A RECEPTOR 3.
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
CYS-RICH.
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ATP (BY SIMILARITY).
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BY SIMILARITY.
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Pred. No. le-
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P29319;
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01-DEC-1992 (Rel. 24, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.1)

KINASE RECEPTOR ETK1) (MEK4).

EPHA3 OR ETK1 OR MEK4 OR TYRO4.
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PRINTS; PRO0109; TYRKINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

PFAM; PF00069; PK1nase; 1.

PFAM; PF00069; SAM; 1.

PFAM; PF00536; SAM; 1.

PFAM; PF01504.
SEQUENCE FROM N.A. STRAIN-ICR X SWISS MEDLINE; 92031278. Sajjadi F.G., Pasqu
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MIM; 17961:
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                                                                                         Mus musculus (Mouse)
Eukaryota; Metazoa;
Eutheria; Rodentia;
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FIBRONECTIN TYPE-III.
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EXTRACELLULAR
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-> L (IN CAA01906).
B8D900FA80FF5121 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY).
                                                                                                                                                                                 update)
: 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RECEPTOR 3. (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                 (TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                             Mammalia
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VNLLDSKTIQGELGWISYPSHG

51

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Query Match
Best Local
                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0014; FNTYPEIII.

PRINTS; PRO0109; TYRKINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

PRAM; PF000041; fn3; 2.

PEAM; PF00005; PKinase; 1.

PFAM; PF000536; SAM; 1.

PFAM; PF00536; SAM; 1.

PFAM; PF00536; SAM; 1.
                                                                                                     CARBOHYD
VARSPLIC
SEQUENCE
                                                                                                                                         CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                             ACT_SITE
MOD_RES
                                                                                                                                                                                                                    NP_BIND
BINDING
                                                                                                                                                                                                                                                                                                                                      CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M68513; AAA39521.1; -.
EMBL; M68515; AAA39522.1; ALT_SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Identification of a new eph-related receptor tyrosine kinase gene from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor.";

New Biol. 3:769-778(1991).

-I- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                             Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGD; MGI:99612; EPHA3
PRINTS; PRO0014; FNTY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A45583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                            TRANSMEM
                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                               Receptor;
                μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: A SECRETED VARIANT WITHOUT THE TRANSMEMBRANE REGION AND THE KINASE DOMAIN IS PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.
TISSUE SPECIFICITY: GREATEST LEVELS OF EXPRESSION OCCURRING IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BRAIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPHRIN-A2, -A3, -A4 AND -A5.
CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEIN TYROSINE PHOSPHATE.
             VNLLDSKTIQGELGWISYPSHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P16109;
  Similarity
22; Conserv
                                                                                                                                                                                                                                                                                                                                                               Transmembrane;
                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                           Tyrosine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A45583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1FSB
                                                                                                      A,
                                                                                                        109955
                                                    100.0%;
                                                                .0%;
                                                                                                                                                                                                                                                                                                                                                   GLycoprotein; Sig
BY SIMILARITY
                                                                                                     MW;
                                                                                                                         BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
                22
                                      0;
                                                                                                                                                                                                        ATP
ATP
BY S
                                                                                                                                                                                                                                                                                                                       EPHRIN TYPE-A RECEPTOR 3. EXTRACELLULAR (POTENTIAL).
                                                                                                                   MISSING
                                                                                                                                                                                                                                                          FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                   CYTOPLASMIC CYS-RICH.
                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                             kinase; ATP-binding; Phosphorylation;
oprotein; Signal; Alternative splicing
                                                     Score 119;
Pred. No. 1
                                                                                                     BE44A6655D8107A2 CRC64;
                                      Mismatches
                                                                                                                                                                                                                    (BY SIMILARITY).
                                                                                                                                                                                                                                               KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no restrictions ong as its content is in
                                                  le-10;
                                                                                                                                                                                                                                                                                               (POTENTIAL)
                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Usage
                                        0;
                                                              Length 983;
                                        Indels
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                                                                                                                                                                                            SIMILARITY)
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                                      Gaps
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EPA3_RAT
008680;
DOMAIN
NP_BIND
BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
                                                                                                                                                                      TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                        Receptor;
                                                                                                                                                                                                                                                                                  PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PFAM; PF00041; fn3; 2.
PFAM; PF00069; pkinase; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF01404; EPH_lbd; 1.
Transferase; Tyrosine-protein kinase; ATP-binding;
                                                                                                                                      DOMAIN
DOMAIN
                                                                                                                                                                                                                          CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIY.Y., MCTIETNAN C.F., Feldman A.M.;
"IL-1 beta alters the expression of the receptor tyrosine kinase gene r-Ephha in neonatal rat cardiomycoytes.";
Am. J. Physiol. 274:H331-H341(1998).
-i- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A2, -A3, -A4 AND -A5.
-i- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
15-FEB-2000 (Rel. 39, Last annotation update)
EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR REK4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RAT
                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U69278; AAC06273.1; -. HSSP; P16109; 1FSB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-SPRAGUE DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 98120505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATA
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                         Transmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                         RECEPTOR_TYR_KIN_V_1; 1.
RECEPTOR_TYR_KIN_V_2; 1.
 license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                         Glycoprotein;
BY SIMILA
POTENTIAL.
                                                                                      ATP
                                                                                                                                                                      POTENTIAL.
CYTOPLASMIC (POTENTIAL)
CYS-RICH.
                                                                                                                                                                                                                    EPHRIN TYPE-A RECEPTOR 3. EXTRACELLULAR (POTENTIAL)
                                               BY SIMILARITY.
PHOSPHORYLATION (AUTO-)
                                                                                                                                   FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III.
                                 POTENTIAL.
                                                                                                                     PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                         SIMILARITY
                                                                                      (BY
                                                                                   SIMILARITY).
                                                                                                                     KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           984
                                                                                                                                                                                                                                                                         Signal.
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                                                                                                                                                                                                                                                                                         Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia;
                                                 (BY SIMILARITY)
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RESULT 5
EPA5_CHICK
         TAREST RESERVATE RESERVATION OF THE PROPERTY O
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Best Local :
                                                                   EMBL: U03910; AABGO612.1; -.
HSSP; P00523; 2PTK,
PRINTS; PRO0014; FNTYPEIII.
PRINTS; PRO0014; FNTYPEIII.
PRINTS; PRO0019; TYRKINASE.ATP; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS00186; EGF_2; UNKNOWN_1.
PFAM; PF00064; FAN; 1.
PFAM; PF00069; PK10aSe; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF00536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                 EMBL; U03910;
EMBL; U03910;
EMBL; U03910;
HSSP; P00523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
SEQUENCE
    Transferase;
Receptor; Tra
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no rest
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or send an email to license@isb-sib.ch).
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01-OCT-1996 (Rel. 34, Last sequence)
01-NOV-1997 (Rel. 35, Last annotati
EPHRIN TYPE-A RECEPTOR 5 PRECURSOR
KINASE RECEPTOR CEK7).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Siever D.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPHA5 OR CEK7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification of a complete Cek7 receptor protein tyrosine kinase coding sequence and cDNAs of alternatively spliced transcripts."; Gene 148:219-226(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPA5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <del>-</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EPHRIN-A1, -A2, -A3, -A4 AND -A5.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED B ALTERNATIVE SPLICING.

SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATA DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.

SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: RECEPTOR FOR MEMBERS EPHRIN-A1, -A2, -A3, -A4 AND -A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VNLLDSKTIQGELGWISYPSHG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity 100
22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95047429.
se: Tyrosine-protein kinase; ATP-binding; Phosphorylation;
Transmembrane; Glycoprotein; Signal; Alternative splicing
1 31 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        404
493
984
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                                                                                                                                                                                                                                                                                                                                                              AAB60613.1; -.
AAB60614.1; -.
AAB60612.1; -.
2PTK.
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110227
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POTENTIAL.
v; F170C49312F7A0AB
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Pred. No. 1e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OF THE EPHRIN-A FAMILY. BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lon update)
 (EC 2.7.1.112) (TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vertebrata; Archosauria;
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                        splicing
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RESULT
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Best Local Similarity 68.:
Matches 15; Conservative
        EMBL; U07357;
HSSP; P00523;
MGD; MGI:99654
                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
EHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.
KINASE RECEPTOR EHK-1) (EPH HOMOLOGY KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
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VARSPLIC
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BINDING
ACT_SITE
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                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                  Zhou R., Copeland T.D., Kromer L.F., Schulz
"Isolation and characterization of Bsk, a g
tyrosine kinase associated with the limbic
J. Neurosci. Res. 37:129-143(1994).
1- FUNCTION: RECEPTOR FOR MABERS OF THE E
EPHRIN-A1, -A2, -A3, -A4 AND -A5.
-1- CATALYIC ACTIVITY: ATP + A PROTEIN TYR
                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                              STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                   EPHA5 OR EHK1 OR CEK7 OR BSK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                   MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                  Eutheria;
                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VNLLDSKTIQGELGWISYPSHG
                                                                                                                                       TISSUE SPECIFICITY: BRAIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CAT DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                             PROTEIN TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
        MGI:99654; EPHAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNLLDSRTVMGDLGWIAYPKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOUSE
                                                                                                                                                                                                                                                                                                     94194581
                                                                                                                                                                                                                                                                                                                                                ; Metazoa; Chordata; Craniata; Vertebrata; Rodentia; Sciurognathi; Muridae; Murinae;
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                               AAA17038.1;
                                                                                                                                                                                                                                                                                                               TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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549
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9123
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665
665
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776
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2412
4437
4437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112245
                                                                                                                                                                                                                               FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS 3, -A4 AND -A5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .28;
                                                                                                                                                                                                                                                                                                                                                                                                         annotation update)
ECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
HOMOLOGY KINASE-1) (BRAIN-SPECIFIC KINA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
POTENTIAL.
POTENTIAL.
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POTENTIAL.
MISSING (IN ISOFORM 2).
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CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCCDHGCGWASSLRAVAYPSLIW -> R (IN ISOFORM 1 AND ISOFORM 2).
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC36FD6AEBF38382 CRC64;
                                                                                                                                                                                                                                                                Schulz N.T.;
sk, a growth factor receptor-like
limbic system.";
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1.1e-06;
                                                                                                                                                                                                                    TYROSINE -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1013
                                                                                                                                                                                                                    ADP
                                                                                                                                                                                                                                                                                                                                                 Mammalia;
Mus.
                                                                                                                                                                       CATALYTIC
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PR00014; FNTYPEIII

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Best Local S
Matches 14
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PROSITE: PS01186; EGF_2; UNK
PFAM; PF00041; fn3; 1.
PFAM; PF00069; PK1nase; 1.
PFAM; PF00536; SAM; 1.
                                                                                                                                                           ALDRESS, CAD be activated by three (Oncogene 14:533-542(1997).
                                                                                                                                                                                                                                                                                       009127;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
FPHRIN TYPE-A RECEPTOR 8 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN EPHRIN TYPE-A RECEPTOR 8 PRECURSOR (EC 2.7.1.112)
                                                                               This SWI
between
                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Futheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NP_BIND
BINDING.
ACT_SITE
CARBOHYD
CARBOHYD
SEQUENCE
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DOMAIN
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SIGNAL
              modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 97178845.
                                                                                                                                                                                                                                                                                                                                                                                                    MOUSE
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PROSITE; PS00107; PROTEIN_K
PROSITE; PS00109; PROTEIN_K
PROSITE; PS50011; PROTEIN_K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VNLLDSKTIQGELGWISYPSHG
||||||:|:|:||||::|:|
63 VNLLDSRTVMGDLGWIAFPKNG
                                                   s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Excurpean Bioinformatics Institute. There are no restriby non-profit institutions as long as its content
                                                                                                                        CATALTIC ACTIVITY: ATP + A PROTEIN TYROSINE = PROTEIN TYROSINE PROSPER FOR TYPE I MEMBRANE PROTEIN. TYPE I MEMBRANE PROTEIN. SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES 1
                                                                                                               DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00536; SAM; 1.
PF01404; EPH_1bd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 63.1
14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane; Glycoprotein;
1 26 BY SIMILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tyrosine-protein kinase; ATP-binding; Phosphorylation
                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26
877
412
433
877
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97115
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RECEPTOR_TYR_KIN_V_2; 1.
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Pred.
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54AD2DC864178214 CRC64;
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                                                                                                                                                            FAMILY
ADP +
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                                                                restrictions
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                                                                           collaboration -
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Best Local S
Matches 14
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PRINTS; PRO00014; FNNYIPEIII.

PRINTS; PRO0109; TYRKINASE.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS001109; PROTEIN_KINASE_TON; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
                                      Basu R., Welcher A.A.; CDNA cloning and tissue distribution protein-tyrosine kinases ";
Oncogene 10:897-905(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                    01-OCT 1996 (Rel. 34, Created)
01-OCT 1996 (Rel. 34, Last sequence update)
10-UL-1998 (Rel. 36, Last annotation update)
15-UL-1998 (Rel. 36, Last annotation update)
EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN-KINASE RECEPTOR EHK-1) (EPH HOMOLOGY KINASE-1) (RECEPTOR PROTEIN-TYROSINE KINASE HEK7).
EYHAD5 OR EHK1 OR HEK7.
HOMO Sapiens (Human).
EDWARYOta; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                                                                        HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BINDING
                                                                                        MEDLINE; 95206782.
Fox G.M., Holst P.
                                                                                                                                              Submitted
                                                                                                                                                                                                                                                                                                    P54756;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM;
PFAM;
PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00790; RECEPTO PROSITE; PS00791; RECEPTO PROSITE; PS01186; EGF_2; PFAM; PF00041; fn3; 2.
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                                                                                                                TISSUE-BRAIN;
                                                                                                                        SEQUENCE OF
                                                                                                                                                      Miescher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                               Eutheria;
                                                                                                                                                                 TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Iransferase; Tyrosine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                               31 VNLLDTSTIHGDWGWLTYPAHG
                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                  1 VNLLDSKTIQGELGWISYPSHG
        FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A1, -A2, -A3, -A4 AND -A5. CATALYTIC ACTIVITY: ATP + A PROTEIN PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                             HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00069; pkinase; 1.
PF00536; SAM; 1.
PF01404; EPH_lbd; 1.
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                                                                                                                                                                                                                                                                                                             STANDARD;
LOCATION: TYPE I MEMBRANE PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          110764
                                                                                        Chute H.T., Lindberg
                                                                                                                                            the EMBL/GenBank/DDBJ databases
                                                                                                                        N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein;
POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW;
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Pred.
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POTENTIAL.
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY
                                                                                                                                                                                              Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        8530E800290FE502 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                No.
                                       THE
                                                                     of five
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; 1
4.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal.
                   TYROSINE -
                                                                                                                                                                                                                                                                                                            A
                                       EPHRIN-A
                                                                                        R.A., Janssen
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                                                                     human
                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1004;
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                                      FAMILY.
                                                                    EPH-like receptor
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Best Local
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BINDING
ACT_SITE
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
PROSITE; PS00101; PROTEIN KINASE_DON;
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entities requires a license agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This
             EPA5_RAT STANDARD; PRT; 1005 AA. P54757; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.1 KINASE RECEPTOR EHK-1) (EPH HOMOLOGY KINASE-1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO0109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <del>-</del>
                                                                                                                  RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED I ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED IN THE INSTITUTE.
SYSTEM.
SYSTEM.
SYSTEM.
TYPO OTHER PROTEIN-TYROSINE KINASES IN THE CATALOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                              φ
                                                                                                                                                                                          VNLLDSKTIQGELGWISYPSHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      600004
                                                                                                                                                                           VNLLDSRTVMGDLGWIAFPKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00041; fn3; 2.
PF00069; pkinase; 1.
PF00536; SAM; 1.
PF01404; EPH_lbd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X95425; CAA64700.1;
L36644; AAA74245.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P00523;
  ဝ္က
                                                                                                                                                                                                                                  14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                Similarity
  EKH1 OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane;
                                                                                                                                                                                                                                                                                                        1037
                                                                                                                                                                                                                                                                                                                                     Conservative
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63
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                                                                                                                                                                                                                                                . 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein;
POTENTIAL.
                                                                                                                                                                           82
                                                                                                                                                                                                    22
                                                                                                                                                                                                                               Score 89; DB
Pred. No. 4.9e
6; Mismatches
                                                                                                                                                                                                                                 6
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MW; FC2C46C959AFB699 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     ATP (BY SIMILA
BY SIMILARITY.
POTENTIAL.
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CYTOPLASMIC (POTENTIAL).
PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPHRIN TYPE-A RECEPTOR EXTRACELLULAR (POTENTIA
                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kinase; ATP-binding; Phosphorylation;
oprotein; Signal; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY SIMILARITY). (BY SIMILARITY).
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4.9e-06;
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CARBOHYD
                                                                      CARBOHYD
CARBOHYD
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TRANSMEM
                                                                                                                              NP_BIND
                                                                                                                                                                                                                                  Receptor;
SIGNAL
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                                                                                                  CARBOHYD
                                                                                                                  ACT_
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                                                                                                                                                                                                                                                                             PFAM;
                VARSPLIC
                                                          CARBOHYD
                                                                                                                                                                           DOMAIN
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Elk-like receptor tyrosine kinase in brain.";

Neuroscience 63:163-178(1994).

-i- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. E

EPHRIN-A1, -A2, -A3, -A4 AND -A5.

-i- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +

PROTEIN TYROSINE PHOSPHATE.

-i- SUBCELIULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-i- SUBCELIULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                             use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a light or comentities and the comentities are considered.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lassmann H., Steck A.J.;
"Expression and developmental regulation of Ehk-1, a Fik-11ke receptor tyrosine kinase in brain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Eutheria; Rodentia; Sciu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN; MEDLINE; 95206467.
                                                                                                                     entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Taylor V., Pfarr S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oncogene 8:3277-3288(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maisonpierre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 94067777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXP
SYSTEM. PREDOMINANTLY EXPRESSED IN NEURONS
                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATY DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
X78689; CAA55357.1;
P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pierre P.C., Barrezueta N.X., Yancopoulos G.D.;
and Ehk-2: two novel members of the Eph receptor-like tyrosine
family with distinctive structures and neuronal expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata;
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Miescher G.C., Honegger P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-BRAIN,
                                                                                                                                                     (See http://www.isb-sib.ch/announce/
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PRINTS; PRO0014; ENTYPEIII.

PRINTS; PRO0109; TYRKINASE.

PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS0011; PROTEIN_KINASE_DOW; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS001791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS001791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS01791; PSC1186; EGF_2; UNKNOWN_1.

PFAM; PE00069; Pkinase; 1. Transferase; PF01404; Transmembrane; 576 577 597 597 709 802 802 802 4425 100 Tyrosine-protein pkinase; 1. EPH_lbd; 1. 1005 575 596 1005 938 691 709 802 266 266 425 438 463 Glycoprotein; POTENTIAL POTENTIAL.

POTENTIAL.

GRRRTQGRGGG -> I

SPLICED FORMS). ATP (BY SIMILAI ATP (BY SIMILAI BY SIMILARITY. POTENTIAL.
POTENTIAL.
POTENTIAL. CYTOPLASMIC (POTENTIAL). POTENTIAL. EXTRACELLULAR (POTENTIAL) EPHRIN TYPE-A POTENTIAL. PROTEIN KINASE kinase; ATP-binding; Phospho: oprotein; Signal; Alternative (BY SIMILARITY). (BY SIMILARITY). RECEPTOR DADGPRAQASWCHARR (IN Phosphorylation;

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Best Local S
Matches 14
                                                                                                        Oncogene 8:1807-1813(1993).

Oncogene 8:1807-1813(1993).

-I- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY.

EPHRIN-A1, -A4 AND -A5. BINDS MORE POORLY TO EPHRIN-A2

-I- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +

PROTEIN TYROSINE PHOSPHATE.

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I- SUBCLEARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAIN.

-I- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CA

DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
                                                                           This SWI
between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPA4_CHICK STANDARD; PRT; 986 AA. 007496; Q90772; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) 01-NOV-1997 (Rel. 35, Last annotation update) EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR CEK8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
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                                                                                                                                                                                                                                                                                                                                             Ando
"The
                                                                                                                                                                                                                                                                                                                                                                      ohta
                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
Neognathae; Galliformes; Phasi
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. TISSUE-SPINAL CORD;
                                                                                                                                                                                                                              expressed."
                                                                                                                                                                                                                                                      MEDLINE; 93288
Sajjadi F.G.,
                                                                                                                                                                                                                                                                                           SEQUENCE OF 138-986 FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPHA4 OR CEK8.
                                                                                                                                                                                                                                         "Five novel avian
                                                                                                                                                                                                                                                                                TISSUE-EMBRYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 VNLLDSKTIQGELGWISYPSHG
                                                         s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                              receptor tyrosine kinase, pes of motoneurons in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VNLLDSRTVLGDLGWIAFPKNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
14; Conserv
                                                                                                                                                                                                                                                                93288394.
                                                                                                                                                                                                                                                                                                                                                       Tanaka H.;
                                                                                                                                                                                                                                                                                                                                                                   Nakamura M., Hirokawa
                                                                                                                                                                                                                                                                                                                                                                                  96404128
                                                                                                                                                                                                                                                                                                                 54:59-69(1996).
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566
578
669
708
979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306
                                                                                                                                                                                                                                                   Pasquale E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΑĄ,
                                                                                                                                                                                                                                       puale E.B.;
Eph-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170
566
578
669
708
979
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111007
                                                                                                                                                                                                                                                                                         z
                                                                                                                                                                                                                                                                                                                                                                                                                                  Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RPPSAPRNAISNVNETSVPLEWIPPADTGGGKDVSYYILCK
KCNSHAGVCEECGGHVRYLPQQIGLKNTSVMADPLAHTNY
TFEIEAVNGVSDLSPGTRQYVSVNVTTNQAA -> T (IN
SPLICED FORMS).

SGSCCECGCGRASSLCAVAHPSLIW -> R (IN
SPLICED FORMS).

D -> E (IN REF. 2).
G -> A (IN REF. 2).
G -> A (IN REF. 2).
G -> A (IN REF. 2).
T -> I (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebraca,
ianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          \begin{array}{lll} {\tt VCRPGFFKASPHSQTCSKCPPHSYTHEEASTSCVCEKDYFR} \\ {\tt RESDPPTMACTR} & -> & {\tt G} & {\tt IN} & {\tt SPLICED} & {\tt FORMS} {\tt )}. \end{array} 
                                                                                                                                                                                                                                         tyrosine
                                                                                                                                                                                                                                                                                                                              Cek8, is transiently expressed spinal cord during development.
                                                                                                                                                                                                                                                                                                                                                                   ×;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                   Tanaka S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1,
9.6e-06;
2;
                                                                                                                                                                                                                                         kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                          Vertebrata; Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                   Iwama
                                                                                                                                                                                                                                         are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                      differentially
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus.
                                                                                                                                                                                                                                                                                                                                                                  Α.,
                                                                                                                         DOMAINS.
THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                   Suda
                                                                       EMBL
                                                                                                                                                                                     BINDS TO
AND A-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                  collaboration
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                                                                       outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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RESULT
EPA4_HU
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Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D38174; BAA07373.1; -.
EMBL; Z19059; CAA79509.1; -.
HSSP; P00523; ZPTK.
PRINTS; PR00104; FNTYPEIII.
PRINTS; PR00109; TYRKIMASE.
PROSITE; PS00107; PROTEIN_KII
PROSITE; PS00109; PROTEIN_KII
PROSITE; PS00109; PROTEIN_KII
PROSITE; PS00790; RECEPTOR_TI
PROSITE; PS00790; RECEPTOR_TI
PROSITE; PS001186; EGF_2; UNKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                EPA4_HUI
P54764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
NP_BIND
BINDBIND
BINDLE
                  Basu R., Welcher A.A.;

"CDNA cloning and tissue distribution of five human EPH-like receptoreDNA cloning and tissue distribution of five human EPH-like receptor FOR Lines.";

Oncogene 10:897-905(1995).

-!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A1, -44 AND -45. BINDS MORE POORLY TO EPHRIN-A2 AND A-3.

-!- CAPALYJIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP +

PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _HUMAN
                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 34, Last annotation update)
EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
KINASE RECEPTOR SEK) (RECEPTOR PROTEIN-TYROSINE KINASE HEK8).
EPHA4 OR SEK OR HEK8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFAM; PF00041; fn3; 2.
PFAM; PF00059; pkinase; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF01404; EPH_1bd; 1.
                                                                                                                                                                       MEDLINE; 95206782.
Fox G.M., Holst P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                          Eutheria;
                                                                                                                                                                                                                                                                                            Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                TISSUE-BRAIN;
                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VNLLDSKTIQGELGWISYPSHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTLLDSRSVQGELGWIASPLEG
                                                                                                                                                                                                                                    FROM
                                                                                                                                                                                                                                                                        ; Metazoa;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tyrosine-protein
                                                                                                                                                                                                                                    N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; PROTEIN_KIMASE_ATF; 1.
; PROTEIN_KIMASE_TYR; 1.
; PROTEIN_KIMASE_DOM; 1.
; RECEPTOR_TYR_KIN_V_1; 1
; RECEPTOR_TYR_KIN_V_2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN_KINASE_TYR;
PROTEIN_KINASE_DOM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGF_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 R
487 S
109482 MW;
                                                                                                                                                                                                                                                                      Chordata; C:
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66.4%;
                                                                                                                                                                       Chute H.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein;
POTENTIAL
TYPE I MEMBRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 79; DB
Pred. No. 0.00
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPHRIN TYPE-A
EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHOSPHORYLATION (AUTO-) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN KINASE.
                                                                                                                                                                                                                                                                      Craniata; Vertebrata; i; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -> G (IN REF. 2).
-> T (IN REF. 2).
BD88C2A5BD840A0F
                                                                                                                                                                       Lindberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
.00017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RECEPTOR 4. (POTENTIAL).
                                                                                                                                                                       R.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
                                                                                                                                                                       Janssen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78)
78)
                                                                                                                                 EPH-like receptor
                                                                                                                                                                                                                                                                                          Mammalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
SIMILARITY).
                                                                                                                                                                       A.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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RESULT 12
EPA4_MOST
ID EPA4_M
AC 003137
DT 01-OCT
DT 01-NOV
DE EPHA4
DE KINASE
GN MUS mu
OC Eukary
OC Eukary
OC Eukary
OC Eukary
OC Eukary
OC EUKARY
RN [1]
RP SEQUEL
RN MEDLII
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                                                                                                                                                                                                     Query Match
Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0014; FNTYPEIII.

PRINTS; PRO0109; TYRKINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

PRAM; PF00041; fn3; 2.

PFAM; PF00041; fn3; 2.

PFAM; PF000536; SAM; 1.

PFAM; PF000536; SAM; 1.

PFAM; PF01404; EPH_1bd; 1.

TIANSferase; TyrOSINe-Protein_kinase; ATP-1
                                                                                     EPA4_MOUSE
Q03137;
Q1-OCT-1994
Q1-OCT-1994
Q1-NOV-1997
                                                                                                                                                                                                                                              NP_BIND
BINDING
BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                   TRANSMEM
DOMAIN
DOMAIN
DOMAIN
                                                                 01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112)
KINASE RECEPTOR SEK) (MPK-3).
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                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MIM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
 SEQUENCE FROM N.A.
STRAIN-C57BL; TISSUE-EMBRYONIC
MEDLINE; 93096484.
                                                           EPHA4 OR SEK.
                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                   31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY:
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN. BELONGS TO THE
                                                                                                                                                                           VNLLDSKTIQGELGWISYPSHG
                                                                                                                                                                  VTLLDSRSVQGELGWIASPLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             602188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L36645;
                                                                                                                                                                                                    Similarity 63.
                                                                                                                                                                                                                                                                        621
627
653
746
779
235
                                                                                                                                                                                                                                                                                                                                   548
570
325
436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA74246.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONTAINS
TO OTHER
                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                               109859
                                                                                                                                                                                                             .68;
                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein;
POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
PROTEIN-TYROSINE KINASES IN THE CATALYTIC
HE EPHRIN RECEPTOR FAMILY.
                                                                                                                                                                                                                                          PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).

BY SIMILARITY (AUTO-) (POTENTIAL).

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.
                                                                                                                                                                                                                                               ₹.
                                                                                                                                                                  52
                                                                                                                                                                                  22
                                                                                                                                                                                                    4:
                                                                                                                                                                                                   Pred. No. 0.00
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                           EPHRIN TYPE-A RECEPTOR 4. EXTRACELLULAR (POTENTIAL). POTENTIAL.
                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III (BY
                                                                                                                                                                                                                                                                                                                                                                                                     kinase; ATP-binding; Phosphorylation;
                                                                                                                        PRT;
         BRAIN
                                                                                                                                                                                                            79;
No.
                                                                                                                       986
                                                                                                                                                                                                                                                                                                                                                                                             Signal.
                                                                                                                                                                                                                    DB 1;
                                  Vertebrata;
ae; Murinae;
                                                                                                                       ₽
                                                                                                                                                                                                              00017
                                                                                                                                                                                                    4.
                                                                                                                                                                                                                   Length 986;
                                                                             (TYROSINE-PROTEIN
                                          Mammalia
                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                restrictions
                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ä
                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n 0
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MGD; MGI:98277; EPHA4.

PRINTS; PRO0014; FNTYPEIII.

PRINTS; PRO0109; TYRKINASE.

PROSITE; PS00109; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00701; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PRAM; PP00041; fn3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X65138;
EMBL; X57241;
EMBL; S57168;
HSSP; P00523;
BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
VARSPLIC
                                                                                                                                                                           DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                          Receptor;
SIGNAL
CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gilardi-Hebenstreit P., Nie
Chestier A., Wilkinson D.G.
Oncogene 8:1103-1103(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gilardi-Hebenstreit P., Nieto M.A., Frain M., Mattei M.-G., Chestler A., Wilkinson D.G., Charnay P.;
"An Eph-related receptor protein tyrosine kinase gene segmentally expressed in the developing mouse hindbrain.";
Oncogene 7:2499-2506(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM;
PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM;
PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERRATUM
                                                                                                                                                                                                                                           NIAMOC
                                                                                                                                                                                                                                                                                      TRANSMEN
                                                                                                                                                                                                                                                                                                                                                                                             Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN ALTERNATIVE PRODUCTS: A SHORTER FORM WITH A DI AMINO ACIDS ALTERING THE CATALYTIC SITE MAY BI ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS EPHRIN-A1, -A4 AND -A5. BINDS MORE POORLY TO EPHRIN-A2 AND A-MAY PLAY A ROLE IN A SIGNAL TRANSDUCTION PROCESS INVOLVED IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LI SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY: HIGHEST LEVELS IN THE HEART, LUNG AND KIDNEY. IT IN THE EMBRYONIC BRAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HINDBRAIN PATTERN FORMATION.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -
                                                                                                                                                                                                                                                                                                                                                                                          pF00056; pkinase; 1.
pF00536; SAW; 1.
pF01404; EBH lbd; 1.
ferase; Tyrosine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93205393
                                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; CAA46268.1; -.; CAA40517.1; -.; AAB25836.1; -.; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N1eto
                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein;
                                                                                                                                                                                                                                                                                                    POTENTIAL.
EPHRIN TYPE-A I
EXTRACELLULAR
                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III (BY
FIBRONECTIN TYPE-III (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    o M.A., Frain M.,
Charnay P.;
                                      PHOSPHORYLATION (AUTO-) (POTENTIAL).
POTENTIAL.
POTENTIAL.
                                                                                                                                             PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                               BY SIMILARITY
                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                      ATP-binding; Phosphorylation; Signal; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S IN THE BRAIN, IS SEGMENTALLY
                                                                                                                                                                                                                                                                                                      RECEPTOR 4. (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INASES IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mattei M.-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DELETION OF 49
BE GENERATED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΑDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAINS.
THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOWER LEVELS
                                                                                                                                                                                                                    SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                        splicing
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D16AD8B85668C80E CRC64; (IN SHORT ISOFORM)

MISSING POTENTIAL

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                        Query Match
Best Local S
Matches 13
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Best Local S
Matches 14
                                                                     NP_BIND
BINDING
ACT_SITE
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                           PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1;
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2;
PROSITE; PS01186; EGF_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996 (Rel. 34, C
01-OCT-1996 (Rel. 34, I
01-NOV-1997 (Rel. 35, I
EPHRIN TYPE-A RECEPTOR
                                                                                                                                                                                                       PFAM;
                                                                                                                                                                                                                        PFAM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPA6_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAT
                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 94067777.
                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
                                                                                                                                  DOMAIN
                                                                                                                                          DOMAIN
                                                                                                                                                   TRANSMEM
                                                                                                                                                            DOMAIN
                                                                                                                                                                             SIGNAL
                                                                                                                                                                                     Receptor;
                                                                                                                                                                                               Transferase;
                                                                                                                                                                                                                                                                                     PRINTS; PRO0109; TYRKINASE
                                                                                                                                                                                                                                                                                              PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPHA6 OR EHK2 OR EHK-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KINASE RECEPTOR EHK-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13
1 VNLLDSKTIQGELGWISYPSHG
                                                                                                                                                                                                                       ; PF00041; fn3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VTLLDSRSVQGELGWIASPLEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNLLDSKTIQGELGWISYPSHG
                                                                                                                                                                                                                                                                                                      P00523;
                                                                                                                                                                                                     PF00069; pkinase;
PF01404; EPH_lbd;
                         l Similarity
13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 63.0
14; Conservative
                                                                                                                                                                                                                                                                                             PR00014; FWTYPEIII.
                                                                                                                                                                                     Transmembrane;
                                                                  409
948
                        Conservative
                                                                                                                                                                                             Tyrosine-protein kinase;
                                                                                                                                                                                                                                                                                                       2PTK
                                                                     ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34, Last sequence update)
35, Last annotation update)
EPTOR 6 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
HK-2) (EPH HOMOLOGY KINASE-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                61.3%;
59.1%;
                                                                     106235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66.4%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                           Glycoprotein;
POTENTIAL.
                                                                     ¥.
                       Score Pred. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 79; DB . Pred. No. 0.007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22
                                                                                             PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
POTENTIAL.
        22
                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                 POTENTIAL
                                                                                                                                                        EPHRIN TYPE-A RECEPTOR 6. EXTRACELLULAR (POTENTIAL).
                                                                             POTENTIAL
                                                                                     POTENTIAL.
                        Mismatches
                                                                    A47DC78EDB2DEF30 CRC64;
                                   No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      948
                                                                                                                                                                                            ATP-binding; Phosphorylation,
                                   0
                                                                                                                                                                                   Signal.
                                          DB 1;
                                .0014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .00017;
                        5.
                                         Length 948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 986
                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia;
Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                        Gaps
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RESERVE AND THE PROPERTY OF TH
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Q62413;
Q1-NOV-1997
                    CHAIN
DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DOMAIN
BIND
BIND
BIND
BIND
BIND
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOUSE
                                                                                                                                                                                                                                                                 Receptor;
                                                                                                                                                                                                                                                                                                                                 PFAM; PF00041; fn3; 2.

PFAM; PF00069; pkinase; 1.

PFAM; PF00536; SAM; 1.

PFAM; PF01404; EPH_lbd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00107; PROTEIN KINASE_ATP;
PROSITE; PS00109; PROTEIN_KINASE_TYR;
PROSITE; PS00101; PROTEIN_KINASE_DOM;
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2
PROSITE; PS01186; EGF_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lee A.M., Navaratnam D., Ichimiya S., Greene M.I., Davis J.G.; "Cloning of m-ehk2 from the murine inner ear, an eph family receptyrosine kinase expressed in the developing and adult cochlea."; DNA Cell Biol. 15:817-825(1996).

-I- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, L
01-NOV-1997 (Rel. 35, L
EPHRIN TYPE-A RECEPTOR
KINASE RECEPTOR EHK-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U58332; AAB53836.1; -. HSSP; P00523; 2PTK. MGD; MGI:108034; EPHA6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPHRIN-A1, -A2, -A3, -A4 AND -A5.
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPHA6 OR EHK2 OR EHK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0014; PRINTS; PRO0109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: TO OTHER PROTEIN-TYBOSINE KINASES IN THE CAT/
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FROM
                                                                                                                                                                                                                                                                                                                                                                                                                     PS50011; PROTEIN_KINASE_DOM; 1.
PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PS01186; EGF_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rodentia;
                                                                                                                                                                                                                                                                                        Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metazoa;
                       Tyrosine-protein kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYRKINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FNTYPEIII.
                                                              1035
549
570
1035
943
644
662
797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata;
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
R 6 PRECURSOR (EC 2.7.1.112)
(EPH HOMOLOGY KINASE-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                     Glycoprotein;
                                                                                                            ATP
                                                                                                                             CYTOPLASMIC (POTENTIAL)
PROTEIN KINASE.
ATP (BY SIMILARITY).
                                         POTENTIAL
                                                              BY SIMILARITY POTENTIAL.
                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                     EPHRIN TYPE-A
EXTRACELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                        (BY SIMILARITY).
(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                 Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                     RECEPTOR 6. (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I., Davis J.G.;
n eph family receptor
adult cochlea.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΑĐΡ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia;
Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         þу
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SEQUENCE

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RESULT
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                                                                                                                    R PRINTS; PRO0014; FNTYPEIII.

R PRINTS; PRO0109; TYRKINASE_ATP; 1.

R PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS00119; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00190; RECEPTOR_TYR_KIN_V_1; 1.

R PROSITE; PS00191; RECEPTOR_TYR_KIN_V_2; 1.

R PROSITE; PS01186; EGF_2; UNKNOWN_1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

R PRAM; PF00041; fn3; 2.

R PFAM; PF00069; pkinase; 1.

R PFAM; PF000536; SAM; 1.

R PFAM; PF01404; EPH_lbd; 1.

R PFAM; PF01404; EPH_lbd; 1.

R PFAM; PF01404; EPH_lbd; 1.
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HSSP; P00523;
MIM; 602190; -
                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "CDNA cloning and tissue distribution of five human EPH-like receptor protein-tyrosine kinases.";
Oncogene 10:897-905(1995).
-i- EUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A1, -A2, -A3, -A4 AND -A5.
-i- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
EPHRIN TYPE-A RECEPTOR 7 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
KINASE RECEPTOR EHK-3) (EPH HOMOLOGY KINASE-3) (RECEPTOR PROTEIN-
TYROSINE KINASE HEK11).
EPHA7 OR EHK3 OR HEK11.
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Basu R., Welcher A.A.;
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TISSUE-BRAIN;
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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34 VYLLDTTTVMGELGWKTYPLNG 55
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SUBGELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARTY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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59.1%;
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                                                                                                               Glycoprotein;
EPHRIN TYPE-A RECEPTOR 7.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
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A38224 Protein-tyrosine kinase (EC 2.7.1 C; Species; Homo sapiens (man) C; Species; Homo sapiens (man) C; Species; Homo sapiens (man) C; Date; 31-Dec-1993 #sequence_rev C; Accession: A38224; B38224 R; Micks, I.P.; Wilkinson, D.; Sal Proc. Natl. Acad. Sci. U.S.A. 89, A; Title: Molecular cloning of HEK A; Reference number: A38224; MUID: A; Accession: A3824 A; Molecule type: mRNA A; Molecule type: mRNA A; Cross-references: GB:M83941; NI A; Experimental source: pre-B-cell A; Cross-references: GB:M83941; NI A; Experimental source: pre-B-cell A; Molecule type: protein A; Molecule type: protein A; Residues: 21-39;810-860 <wiz> C; Superfamily: protein-tyrosine k C; Keywords: ATP; autophosphorylat C; Keywords: ATP; autophosphorylat C; Keywords: ATP; autophosphorylat F;1-20/Domain: Signal sequence #s</wiz>	Query Match Best Local Similarity 100.0% Matches 22; Conservative Qy 1 VNLLDSKTIQGELGWISYPSHG	RESULT 1 B45583 receptor tyrosine kinase Cek4 - chicken C; Species: Gallus gallus (chicken) C; Species: Gallus gallus (chicken) C; Species: Gallus gallus (chicken) C; Date: 22-Apr.1993 #sequence_revision 18 C; Accession: B45583 R; Sajjadi, F. G.; Pasquale, E.B.; Subraman New Biol. 3, 769-778, 1991 A; Title: Identification of a new eph-rela A; Reference number: A45583; MUID:92031278 A; Accession: B45583 A; Status: preliminary A; Molecule type: mRNA A; Accession: B45583 A; Residues: 1-983 < SAJ> A; Cross-references: GB:M68514; NID:945480 A; Cross-references: GB:M68514; NID:945480 A; Mote: sequence extracted from NCBI back C; Superfamily: protein tyrosine kinase, C; Keywords: ATP; autophosphorylation; pho F; 619-885/Domain: protein kinase ATP-bind		31 53 44.5 976 32 52 43.7 1006 33 49 41.2 368 34 48 40.3 1763 35 48 40.3 1763 36 47 39.5 967 47 39.5 967 48 46 38.7 457 40 46 38.7 457 40 46 38.7 746 41 45 37.8 530 43 37.8 619 44 37.0 234
2.7.1.112) hek precursor - human): repression 31-Dec-1993 #text_change 18-J ; Salvaris, E.; Boyd, A.W. 1. 89, 1611-1615, 1992 if HEK, the gene encoding a receptor tyro MUID:92179233 MUID:92179233 rom NCBI backbone (NCBIP:86627) II2> sine kinase, receptor type eph; fibronect rylation; glycoprotein; phosphoprotein; ce #status predicted <sig></sig>	0%; Score 119; DB 2; Length 9 0%; Pred. No. 1.4e-10; 0; Mismatches 0; Indels HG 22 	ted receptor tyros ted receptor tyros ted receptor tyros (NCBIN:AAA48666.1 pp pIDN:AAA48666.1 pone (NCBIN:62405,	ALIGNMENTS	2 A36355 kin 2 JC5526 kin 2 C70809 hyp 2 T19184 hyp 2 C65088 8 A18 2 G718678
ge 18-Jun-1999 or tyrosine kinase expre PID:g183932 oronectin type III repea	983; 0; Gaps 0;	ange 18-Jun-1999 ine kinase gene from mouse NCBIP:62411) fibronectin type III repea membrane protein		protein-tyrosine k kinase-defective E hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote alaninetRNA liga hypothetical prote eIF-4A-like DEAD f CSD3 protein - yea hypothetical prote capsid protein - N translation elonga myosin I, high mol hypothetical prote

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A, Status: preliminary
A, Molecule type: mRNA
A; Residues: 1-983 <SAJ>
A; Cross-references: GB:M68513; NID:g199119; PIDN:AAA39521.1; PID:g199120
A; Cross-references: GB:M68513; NID:g199119; PIDN:AAA39521.1; PID:g199120
A; Note: sequence extracted from NCBI backbone (NCBIN:62398, NCBIP:62401)
C; Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin ty
C; Keywords: ATP: autophosphorylation; phosphoprotein; transmembrane prote
F; 619-885/Domain: protein kinase homology <KIN>
F; 627-635/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             receptor tyrosine kinase Mek4 - mouse C;Species: Mus musculus (house mouse) C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change C;Accession: A45583 R;Sajjadi, F.G.; Pasquale, E.B.; Subramani, S. New Biol. 3, 769-778, 1991
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-279,444-572,'R',596-1013 <SI3>
A;Cross-references: EMBL:U03910; NID:g555617;
                                                                                                A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-572, 'R',596-1013 <SI2>
A;Cross-references: EMBL:U03910; NID:g555617;
                                                                                                                                                                                                                                                                                                                                                                                      receptor-type protein-tyrosine kinase Cek7, C;Species: Gallus gallus (chicken) C;Date: 13-Sep-1996 #sequence_revision 13-Se C;Accession: I50615; I50616; I50614
                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-1013 <SIE>
A; Cross-references: EMBL:U03910; NID:g555617;
A; Accession: I50616
                                                                                                                                                                                                                                                                                     A; Title: Identification of a complete Cek7
A; Reference number: I50614; MUID:95047429
A; Accession: I50615
                                                                                                                                                                                                                                                                                                                                                  R;Slever, D.A.; Verderame, M.F.
Gene 148, 219-226, 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Identification of a new eph-related receptor A; Reference number: A45583; MUID: 92031278
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                                                                                    A; Accession: I50614
                                                                                                                                                                                                                                                                  A; Status: translated from
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Best Local S
Matches 22
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Best Local S
Matches 22
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Similarity 100.0%;
22; Conservative
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22; Conserv
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llarity 100.0%;
Conservative
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Pred. No. 1.4e-10;
; Mismatches 0;
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Pred. No. 1.4e-10;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                               receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                   long splice
    PIDN: AAB60614.1;
                                                                                                    PIDN: AAB60613.1;
                                                                                                                                                                                                       PIDN: AAB60612.1;
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    PID: g555620
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receptor protein-tyrosine kinase - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 18-Jun-1999
C;Accession: 178843
R;Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, Oncogene 10, 897-905, 1995
A;Title: cDNA cloning and tissue distribution of five human EPH-like receptor, Reference number: IS8351; MUID:95206782
C;Superfamily: protein-tyrosine kinase, re E;627-893/Domain: protein kinase homology F;916-982/Domain: SAM homology <SAM>
                                                                                                                                                                                                                                                                                                                                           RESULT
178843
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C/Reywords: ATP; transmembrane protein
F;512-778/Domain: protein kinase homology <KIN>
F;520-528/Region: protein kinase ATP-binding motif
F;801-868/Domain: SAM homology <SAM>
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C; Superfamily: protein-tyrosine kinase, receptor type eph;
C; Seywords: alternative splicing; ATP; transmembrane protei
F; 649-915/Domain: protein kinase homology <KIN>
F; 657-665/Region: protein kinase ATP-binding motif
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C;Superfamily:
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A; Cross-references: EMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                brain-specific kinase - mouse
C;Species: Mus musculis (house mouse)
C;Date: (02-Jul-1996 #sequence_revision
C;Accession: I48967
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A; Residues: 1-991 < RES>
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                                                         A; Gene: HEK7
                                                                                            A; Cross-references: GB:L36644; NID:g551611; PIDN:AAA74245.1;
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Best Local S
Matches 14
                                                                            Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                  63
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37 VNLLDSRTVMGDLGWIAYPKNG
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68.2%;
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Pred. No. 1.7e
5; Mismatches
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Pred. No. 6.26
6; Mismatches
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                       KIN>
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1.7e-06;
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6.2e-06;
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Query Match

Score

9;

DB 2;

Length 991;

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A;Molecule type: mRNA
A;Residues: 1-898 <TAY>
A;Residues: 1-898 <TAY>
A;Cross references: EMBL:X78689; NID:g531543; PIDN:CAA55357.1;
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibr
C;Keywords: ATP; transmembrane protein
F;568-834/Domain: protein kinase homology <KIN>
F;576-584/Region: protein kinase ATP-binding motif
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R:Taylor, V.; Pfarr, S.; Mi
submitted to the EMBL Data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor tyrosine kinase - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross references: EMBL:S68028
A;Note: the authors translated the codon GAC for residue 170 as Glu A;Note: the authors translated the codon GAC for residue 170 as Glu C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronect C;Keywords: ATP; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Maisonpierre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D. Oncogene 8, 3277-3288, 1993
A;Title: Ehk-1 and Ehk-2: two novel members of the Eph re A;Reference number: S49015; MUID:94067777
A;Accession: S51603
                                      RESULT
S51604
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C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999
C:Accession: S51603
receptor-like tyrosine kinase Ehk-1 - rat C; Species: Rattus norvegicus (Norway rat)
   C; Species:
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A; Residues: 1-893 <MAI>
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Best Local S
Matches 14
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Best Local
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                                                                                                           1 VNLLDSKTIQGELGWISYPSHG 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expression and developmental regulation of EHK-1, a
                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                       Score 87;
Pred. No.
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1.3e-05;
2;
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A; Molecule type: mRNA
A; Residues: 1-305, 'G', '359-1005 <MA2>
A; Cross-references: EMBL: $68026
A; Note: the authors translated the codon GAC for re C; Superfamily: protein-tyrosine kinase, receptor ty C; Keywords: ATP; transmembrane protein F; 675-941/Domain: protein kinase homology <KIN>F; 683-691/Region: protein kinase ATP-binding motif
                                                          receptor tyrosine kinase - African clawed C;Species: Xenopus Laevis (African clawed C;Date: 13-Sep-196 #sequence_revision 13-C;Accession: I51549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                receptor tyrosine kinase Ehk-1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999
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S49015
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R;Maisonpierre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A;Title: Ehk-1 and Ehk-2: two novel members of the Eph re
A;Reference number: S49015; MUID:94067777
A;Accession: S51604
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A;Note: the authors translated the codon GAC for C;Superfamily: protein-tyrosine kinase, receptor C;Keywords: ATP; transmembrane protein
                      R; Winning, R.S.; Sargent, T.D. Mech. Dev. 46, 219-229, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Note: the authors translated A; Accession: S51602
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R;Malsonplerre, P.C.; Barrezueta, N.X.; Yancopoulos,
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A; Residues: 1-981 <MAI>
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    A; Title: Pagliaccio, a member
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A; Residues: 1-1005 <MAI>
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63 VNLLDSRTVLGDLGWIAFPKNG
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63.6%;
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A;Cross-references: EMBL:X65138; NID:g54083; PIDN:CAA46268.1; PID:g54084
R;Gilardi-Hebenstreit, P.; Nieto, M.A.; Frain, M.; Mattei, M.G.; Chestier, A.; W
Oncogene 7, 2499-2506, 1992
A;Title: An Eph-related receptor protein tyrosine kinase gene segmentally expres:
A;Reference number: 330496; MUID:93096484
A;Accession: 530505
A;Molecule type: mRNA
A;Residues: 1-31.55-986 <GIL>
A;Residues: 1-31.55-986 <GIL>
A;Residues: 1-31.55-986 <GIL>
A;Residues: 1-31.55-986 <GIL>
C;Genetics:
C;Genetics:
C;Genetics:
C;Genetics:
C;Genetics:
C;Genetics:
ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotrans:
F;16-596/Product: protein-tyrosine kinase, receptor type eph; fibronectin type III:
C;Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotrans:
F;16-596/Product: protein-tyrosine kinase predicted <MAT>
F;548-569/Domain: transmembrane #status predicted <TMM>
F;548-569/Domain: protein kinase homology <KIN>
F;619-885/Domain: protein kinase homology <KIN-
F;035-7657-Region: protein kinase homology <KIN-
F;035-340,408,423/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;305-340,408,423/Binding site: carbohydrate (Asn) (covalent)
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A;Accession: I51549
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-985 <WIN>
A;Cross-references: GB:L26099; NID:9416402; PIDN:AAA6.
C;Genetics:
A;Gene: Pag
C;Superfamily: protein-tyrosine kinase, receptor type
C;Reywords: ATP; transmembrane protein
F;618-884/Domain: protein kinase homology <KIN>
F;628-634/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein-tyrosine kinase (EC 2.7.1.112) Ep C; Speckes: Mus musculus (house mouse) C; Date: 19-Nov-1997 #sequence_revision 05 C; Accession: S78059; S30505; I58366 R; Charnay, P. submitted to the EMBL Data Library, March A; Reference number: S78059 A; Accession: S78059 A; Accession: S78059 A; Residues: 1-986 < CHA>
  receptor protein-tyrosine kinase - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 18-Jun-1999
C;Accession: I78844
R;Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, P.A.
                                                                                                      RESULT
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Pred. No. 0.00
4; Mismatches
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    Welcher
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A; Gene: HEK11
C; Superfamily: |
C; Keywords: ATP
F; 631-897/Domai
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I58351
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A; Accession: S51605
A; Status: preliminar
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S51605
                                                                            A;Cross-references:
C;Genetics:
                                                                                                                                                                         A; Reference number: A; Accession: I58351
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Keywords: ATP; 1631-897/Domain:
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transmembrane pr
protein kinase
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receptor protein-tyrosine kinase - human (Species: Homo sapiens (man) (2-Jul-1996 #text_change 18-Jun-1999 (2-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999 (2-Accession: I58351 R.F.D.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, Oncogene 10, 897-905, 1995 Oncogene 10, 897-905, 1995 A;Title: cDNA cloning and tissue distribution of five human EPH-like recept A;Reference number: I58351; MUID:95206782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-948 < MAI>
A; Cross references: EMBL: 568030
A; Cross references: EMBL: 568030
C; Superfamily: protein-tyrosine kinase,
C; Keywords: ATP; transmembrane protein
F; 628-936/Domain: protein kinase homolog
F; 636-644/Region: protein kinase ATP-bin
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C;Genetics:
A;Gene: HEX8
C;Superfamily: protein-tyrosine kinase, re
F;619-885/Domain: protein kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oncogene 10, 897-905, 1995
A;Title: CDNA cloning and tissue distribution of five A;Reference number: I58351; MUID:95206782
A;Accession: I78844
A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA
A;Residues: 1-986 <RES>
                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-998 <RES>
A;Cross-references: GB:L36642; NID:g551607; PIDN:AAA74243.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Maisonpierre, P.C.; Barrezueta, N.X.; Yancopoulos, Oncogene 8, 3277-3288, 1993
A;Title: Ehk-1 and Ehk-2; two novel members of the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor-like tyrosine kinase Ehk-2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change
C;Accession: S51605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   628-936/Domain: protein kinase homology <KIN>636-644/Region: protein kinase ATP-binding mo
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$49015; MUID:94067777
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4; Mismatches
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                                                        PID: 9551608
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Title: Perfect score: Sequence:

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Scoring table:

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Total number of hits satisfying chosen parameters:
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Listing first 45 summaries
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1: /cgn2_6/ptodata/;
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4: /cgn2_6/ptodata/;
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length: 1000000
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/cgn2_6/ptodata/2/1aa/6_COMB.pep:*
/cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/1aa/Packfiles1.pep:*
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   US-08-673-789-4
US-08-162-809-16
US-08-167-919a-10
US-08-449-645a-21
US-08-702-367a-21
US-08-702-367a-30
US-08-449-645a-30
US-08-673-789-2
US-08-449-645a-13
US-08-702-367a-13
US-08-702-367a-13
US-08-449-645a-13
US-08-469-537a-103
US-08-469-537a-17
US-08-469-537a-17
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PCT-US95-04681-17
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Sequence 4, Appli Sequence 10, Appl Sequence 11, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 30, Appl Sequence 30, Appl Sequence 13, Appl Sequence 13, Appl Sequence 2, Appli Sequence 13, Appl Sequence 13, Appl Sequence 15, Appl Sequence 29, Appl Sequence 101, Appl Sequence 117, Appl Sequence 17, Appl Sequence 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             printed,
                                                                                      ; LENGTH: 982;
; TYPE: AMINO ACID
; STRANDEDNESS: UNKNO
; TOPOLOGY: UNKNOWN
US-08-673-789-4
                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,789
FILING DATE:
CLASSIFICATION EATA:
APPLICATION NUMBER: 08/177,812
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 3026-410
TELECOMMUNICATION INFORMATION:
TELEFAN: (212) 758-4800
TELEFAN: (212) 758-4800
TELEFAN: (212) 751-6849
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
FENCHTH: 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-673-789-4
 Query Match
Best Local S
Matches 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ZHOU, RENPING; SCHULZ, APPLICANT: T.; KROMER, LAWRENCE, APPLICANT: GEORGE, F.
TITLE OF INVENTION: BSK RECEPTOR TITLE OF INVENTION: USE IN DIAGNOUT OF INVENTION: WITHOUS NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN STREET: 345 PARK AVENUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: MORGAL
STREET: 345 PARK
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNKNOWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BSK RECEPTOR LIKE
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PCT-US96-00419-2
US-08-673-789-6
US-08-426-226-2
US-08-449-645A-11
US-08-673-789-9
US-08-702-367A-19
PCT-US95-04681-11
US-08-702-367A-19
PCT-US95-04681-19
US-08-162-809-18
US-08-162-809-18
US-08-162-809-12
US-08-449-645A-20
US-08-702-367A-20
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Score 119; DB 2;
Pred. No. 1.7e-10;
; Mismatches 0;
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Result

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Score

Length 982; Indels

0;

Gaps

0

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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/162,809
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 9-LJ 9503
REFERENCE/DOCKET NUMBER: P-LJ 9503
FELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
TYPE: amino acids
TYPE: amino acids
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US-08-162-809-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: US-08-162-809-16
                                                                                                                                                                                                                                           Sequence 10, Applicat Patent No. 5674691 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No. 5457048 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/08162809 Patent No. 5457048
CORRESPONDENCE ADDRESS:
CORRESPONDENCE Scully, Scott, Murphy & Presser
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 43, CITY: San Diego
CITY: San Diego
CTATE: California
"nited St
                                                                         APPLICANT: Boyd, Andrew W.
APPLICANT: Simpson, Richard J.
APPLICANT: Wicks, Ian
APPLICANT: Wicks, Ian
APPLICANT: Wilkinson, David
TITLE OF INVENTION: AND USE THEREOF
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL AND FLORES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: PASQUALE, ELENA B.
APPLICANT: Sajjadi, Fereydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                            29 VNLLDSKTIQGELGWISYPSHG 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 119; DB 1; 100.0%; Pred. No. 1.7e-10; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 983;
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 21, Application US/08449645A Patent No. 5981245
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION UMBER: PK9992 (AU)
FILING DATE: 12-DEC-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AL
FILING DATE: 19-JUN-1992
ATTORNEY_AGENT INFORMATION:
NAME: DIG19110, Frank S.
REGISTRATION NUMBER: 31,34
                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
                                                                                                                                                                                                                                                                                                 APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PATENTIA RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein
                                                                                                                                                                                                                   ADDRESSEE: Amgen Patent Operations/RBW STREET: 1840 Dehavilland Drive CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 VNLLDSKTIQGELGWISYPSHG 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/O FILING DATE: 18-APR-1994
CLASSIFICATION: 435
                                                                                                                                                                                   COUNTRY: UZIP: 91320
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ER: 9159
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RESULT 6
US-08-715-106-10
Sequence 10, Application US/08715106
Patent No. 6020306
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                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein
US-08-702-367A-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 22; Conservative
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Best Local
                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION: APPLICANT: Fox, G
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SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: EPH-Like TITLE OF INVENTION: Kinases NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Amgen Pat
                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435
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STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 983 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                   30 VNLLDSKTIQGELGWISYPSHG 51
                                                                                                                   1 VNLLDSKTIQGELGWISYPSHG 22
                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                       LENGTH:
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22; Conservat
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VENTION: EPH-Like Receptor Protein Tyrosine
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Pred. No. 1.7e-10;
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Pred. No. 1.7e-10;
                                                                                                                                                                 Mismatches
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RESULT 7
PCT-US95-04681-21
; Sequence 21, Application PC/TUS9504681
; GENERAL INFORMATION:
; APPLICANT: Fox, Gary M.
; APPLICANT: Fox, Gary M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILING DATE: 21-JUN-1991
PRIOR APPLICATION NUMBER: PK9992 (AN APPLICATION NUMBER: PK9992 (AN APPLICATION NUMBER: PCT/AU92/NETION APPLICATION NUMBER: PCT/AU92/NETION APPLICATION NUMBER: PCT/AU92/NETION NUMBER: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 10
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APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOI
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EpH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 983 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,919
FILING DATE: 18-APR-1994
APPLICATION NUMBER: PK6841 (AU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U$/08/715,106
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
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                                                                                                                                                                                                             STREET: 400 Garden
CITY: Garden City
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Boyd, Andrew W.
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                                                                                                                                                                                                                                                                                                                                          Length 983;
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CORRESPONDENCE ADDRESS:

ADDRESSEE:

E: Amgen Patent Operations/RBW 1840 Dehavilland Drive

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TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-04681-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-2
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS,
APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
APPLICANT: GEORGE, F.

TITLE OF INVENTION: BSK RECEDTOR LIKE
TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AN
TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPE
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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Matches 22; Conservat
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                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/673,789
ETLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/1
FILING DATE: 04-JAN-1994
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US95/04681
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                                                                                                                                                                                                                                                                                                                                                                                        NEW YORK
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California
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ilarity 100.0%;
Conservative (
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TYROSINE KINASE AND LIGAND AND THEIR
USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
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                                                                                                                                      08/177,812
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                                          2026-4105
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Pred. No. 1.7e-10;
D; Mismatches 0;
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US-08-702-367A-30
; Sequence 30, Application US/08702367A
; Patent No. 5981246
; GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 877
TYPE
                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: 1
INFORMATION FOR SEQ ID NO: 30-
SEQUENCE CHARACTERISTICS:
LENGTH: 967 amino acids
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GENERAL INFORMATION:
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Best Local :
                                                                                                                                                                              Matches
                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: sinc
TOPOLOGY: linear
MOLECULE TYPE: prote
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
APPLICANT: Fox, Gary M.
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STRANDEDNESS: UNKNOWN
                                                                                                                                 1 VNLLDSKTIQGELGWISYPSHG
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o. 5981245
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Similarity 63.6%;
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1840 Dehavilland Drive
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63.6%;
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Pred. No. 6.8e-06;
                                                                                                                                                                                       Score 89; DB 2;
Pred. No. 7.6e-06;
                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                      Length 967;
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RESULT 11
US-08-449-645A-13
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                           REFERENCE/DOCKET NUMBER: A INFORMATION FOR SEQ ID NO: 13: SEQUENCE CHARACTERISTICS:
                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 967 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                              NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: EPH-Like TITLE OF INVENTION: Kinases NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VNLLDSKTIQGELGWISYPSHG 22
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13 VNLLDSRTVMGDLGWIAFPKNG 34
                                                                                                                                  APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                              ADDRESSEE: Angen Patent Operations/RBW
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
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CLASSIFICATION: 435
                                                                                                               CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                 ZIP: 91320
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Local Similarity 63.6%;
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F: 1840 Dehavilland Drive
Thousand Oaks
             991 amino acids
amino acid
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linear
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Pred. No.
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-702-367A-13
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US-08-702-367A-13
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                                                                     Sequence 13, Application PC/TUS9504681
GENERAL INFORMATION:
APPLICANT: FOX, GATY M.
TITLE OF INVENTION: EPH-Like RecepTITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 28
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Best Local Similarity
Matches 14; Conserv
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Patent No. 5981246
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,367A
                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 991 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: FOX, GATY M.
TITLE OF INVENTION: EPH
TITLE OF INVENTION: Kin
NUMBER OF SEQUENCES: 43
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CITY: Thousand Oaks
STATE: California
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ZIP: 91320
                             STREET:
                                         ADDRESSEE:
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Thousand Oaks
California
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                          E: Amgen Patent Operations/RBW 1840 Dehavilland Drive
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63.6%;
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63.6%;
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                                                                                                                                                                                                                         58
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Pred. No.
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7.8e-06;
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7.8e-06;
                                                                                                                                                                                                                                                                                                           Length 991;
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Best Local S
Matches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
                                                     TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                 REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 921
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/25-8674
TELEPAX: 415/952-9881
                                                                                                                                                                       APPLICATION NUMBER: 08/3
FILING DATE: 27-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia "1----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04681
                SEQUENCE CHARACTERISTICS:
LENGTH: 928 amino acid
                                                                                                                                                                                                                  FILING DALL:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/330128
                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS: ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08
FILING DATE: 15-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 74.8%;
Local Similarity 63.6%;
les 14; Conservative
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TOPOLOGY: linear
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South San Francisco
amino acid
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              928 amino acids
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                                                     2:
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; TYPE: ami
; TOPOLOGY:
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                                                                           Query Match
Best Local s
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APPLICATION NUMBER: US/08/440
FILLING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UDMBER: 08/330128
FILLING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: TOTCh1a, Timothy E.
REGISTRATION NUMBER: 35,700
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 928 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 92.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEPHAX: 415/952-9881
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MEDIUM TYPE: 5.25 Inch, 360 Kb:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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63.6%;
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                                                           Score 87; DB 1;
Pred. No. 1.5e-05;
6; Mismatches :
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Copyright (c) 1993 - 2000 Compugen
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Penicillium purpur
Penicillium purpur
Small round virus
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Eph-related PTK Ce
Mouse Bsk receptor
EPH-like receptor
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07-JAN-1993.
19-JUN-1992. AU0294.
21-JUN-1991. AU-006841.
12-DEC-1991. AU-009992.
(HALL-) HALL INST MEDICAL RE(
CHALL-) Simpson R, Ward Li
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Claim 6; Fig 1; 58pp; English.
This sequence represets human eph/elk-like kinase (HEK). HEK is expressed in both pre-B cells and T cell lines and in a number of tumours of human origin, eg. lymphoid tumours LK63, Lila-1 and JM, and the epithelial tumour HELA. This receptor-type thymidine kinase and the epithelial tumour HELA.
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R31466;
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                                                                                                                     Receptor-type tyrosine kinase reactive with monocional antibody III-A4 - is EPH-ELK-like kinase, useful for phosphorylating proteins in modulating pre-B, B and T cell function, in cancer
 (TK) and/or
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                                                                                                                                                                                                                                                                                                                                                                                                          "ATP binding site"
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Scoring table: Sequence: Title: Perfect score:

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29-SEP-1998.
11-JUN-1996; 673789.
04-JAN-1994; US-177812.
11-JUN-1996; US-673789.
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Gallus sp.
WO9515375-A.
                                                                                                                                                                                                                                                Mouse Bsk receptor-like tyrosine kinase.

Mouse; Bsk; receptor-like tyrosine kinase; brain; diagnosis; neoplasm; neurodegenerative disease; limbic system neuron regeneration; chromosomal abnormality; degenerative growth; development disorder; viral infection; bacterial infection; Alzheimer's disease; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 85-89; 129pp; English.

Probes derived from the EPH-related PTKs Cek4 (Q90659) and Ce (Q90660) were used to isolate novel cDNA clones (Q90652-58, Q90661-62) from chicken embryo and embryonic brain libraries. Cek4 is highly expressed in the chicken developing brain and embryonic tissues and also in the adult brain and retina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pasquale EB, Sajj
WPI; 95-215256/28.
N-PSDB; Q90659.
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                        (SCHU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-JUN-1995.
07-SEP-1994; U10140.
03-DEC-1993; US-162809.
(LJOL-) LA JOLLA CANCER RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eph-related PTK Cek4. Cek4; Eph; protein ty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R75711 standard; Protein; 983
                                                                                                                                                                                                                                 schizophrenia;
                                                                                                                                                                                                                                                                                                                                                                     25-NOV-1998 (first
                                                                                                                                                                                                                                                                                                                                                                                                                   W71628 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eph-related protein tyrosine kinase(s) -
                                                                        (KROM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L1-NOV-1995
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Local (
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) KROMER L F.
) SCHULZ N T.
) WOUDE G F V.
ZHOU R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . Similarity
22; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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983 AA;
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                                                                                                                                                                                                                                 stroke;
                                                                                                                                                                                                                                                                                                                                                                     entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50
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Pred. No. 1.1e-10;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 119; DB 1;
Pred. No. 1.1e-10;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for monitoring and diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 983;
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                                   Claim 18; Page 54-57; 133pp; English.

Claim 18; Page 54-57; Page 10; Page 11; Page 11; Page 11; Page 11; Page 12; Page 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents mouse Bsk, which is a receptor-like tyrosine kinase. The nucleic acid sequence encoding Bsk can be used in Bsk nucleic acid probes, which can be used in detecting alterations in the level of Bsk messenger-RNA (mRNA) in biological samples isolated from a mammal afflicted with a disease, such as neurodegenerative diseases or disorders and neoplasms. The nucleic acid sequence can all be delivered into the limbic system of patients with limbic system neurodegenerative disease, disorder or injury, to promote or enhance limbic system neuron regeneration or growth. Such neurodegenerative diseases include, chromosomal abnormalities, degenerative growth and development disorders, viral infections, bacterial infections, brain injuries, neoplastic conditions, Alzheimer's disease, epilepsy, schizopheratics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid sequence encoding protein - used in nucleic acid probes, used in detecting alterations in lever messenger-RNA in biological samples isolated from mammal a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kromer LF, Schulz NT, Woude GFV, WPI; 98-541751/46.
N-PSDB; V58192.
                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid encoding EPH-like receptor tyrosine kinase(s) and related vectors, host cells, proteins, antibodies etc., us diagnostically and therapeutically to modulate receptor activa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPH-like receptor protein tyrosine kinase HEK7 EPH-like receptor protein tyrosine kinase; PTK human eph-like kinase; therapy; diagnosis; vec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    schizophrenia,
Sequence 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-OCT-1995.
14-APR-1995; U04681.
15-APR-1994; US-229509.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AMGE-) AMGEN INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3M, Jing S,
95-373799/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; Protein; 991
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  cells.
991 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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AA;
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Pred.
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5.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vector; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTK; HEK7;
                                                                                                                                                                                                                                                                                                                                                                                                                   ibodies etc., used receptor activation
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RESULT WB 3147 ID WF 3147 ID WF 3147 ID WF 3147 ID WF 314 ID WF 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The AL-1 neurotrophic factor, an eph-tyrosine kinase ligand - used in treatment and diagnosis of neuronal disorders and angiogenesis-related conditions.

The angiogenesis-related conditions.

Example 1; Page 50-53; 75pp; English.

Creat REK7 (R97853) is an eph-related tyrosine kinase receptor, for which AL-1 (see also W97854) is a ligand. Its amino acid sequence which AL-1 (see also W97854) is a ligand. Its amino acid sequence considered from a cDNA clone (T18893) isolated from a hippocampal cDNA library. An REK-IgG fusion was used to screen cultured cell lines for surface expression of REK7-binding activity. Primers considered ligands were used to amplify human breast carcinoma BT20 cell cDNA, and an amplified fragment was used to screen a human contains and considered ligands were used to amplify human breast carcinoma breast carcinoma BT20 cell cDNA, and an amplified fragment was used to screen a human contains and considered ligands were used to amplify human breast carcinoma BT20 cell cDNA, and an amplified fragment was used to screen a human contains and considered ligands were used to amplify human breast carcinoma BT20 cell cDNA, and an amplified fragment was used to screen a human contains and conta
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Best Local
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Matches
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   01-DEC-1998.
06-JUN-1995;
17-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-OCT-1995;
27-OCT-1994;
07-JUN-1995;
                                                                                                                                         Rat receptor tyrosine kinase Ehk-1.

Receptor tyrosine kinase; Ror-1; Ror-2; Ehk-1; Ehk-2; neurotrophin activity; trkB; proto-oncogene; tyrosine binding protein; BDNF; NT-3; diagnosis.
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(T18897).
                                                                                        Rattus sp.
US5843749-A.
                                                                                                                                                                                                                                                                                              W83147 standard;
W83147;
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-1994; US-330128.
-1995; US-486449.
) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         928
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469537.
US-406247.
                                                                                                                                                                                                                                                                (first entry)
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                                                                                         domain and Ig constant domain, useful for studying, and therapeutic modulation of, cell growth and differentiation
Disclosure; Page 95-99; 125pp; English.
DNA probes based on protein tyrosine-kinase (pTK) sequences were used to screen cDNA libraries to identify novel pTK genes. The bpTKS, bpTK3, bpTK4, bpTK5 and bpTK7 (R85924-28 and R85935, respectively) are expressed in human brain tissue and show homology to known pTKs. A full-length sequence for bpTK7 (R85936) was also obtd. bpTK7 can be used to design drugs that modulate pTK activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-JUL-1991;
28-OCT-1993;
06-JUN-1995;
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04-APR-1995;
04-APR-1994;
                                                                                                                                                                                                                                                          (GETH )
Bennett
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Example; Fig 22; 194pp; English.
Example; Fig 22; 194pp; English.
Example; Fig 22; 194pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes nucleic acid molecules for ror-1, ror-2, ehk-1 and ehk-2. Also described are the corresponding profeor-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor tyrosine kinases. The present sequence represents rat Ehk-1.
                                                                                      obtd. bpTK7
Sequence 9
                                                                                                                                                                                   Agonist antibodies which activate specific protein tyrosine kinase(s) - also activate chimeric proteins of kinase extracellular domain and Ig constant domain, useful for studying, and therapeutic
                                                                                                                                                                                                                                                                                                                 W09527061-A1.
                                                                                                                                                                                                                                                                                                                                                                                                       peptide
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Maisonpierre PC, Masiakowski P,
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US-469537.
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NTECH INC.
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Best Local S
Matches 14
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06-JUN-1995; 469537.

17-MAR-1995; US-406247.

26-JUL-1991; US-736559.

28-OCT-1993; US-144992.

06-JUN-1995; US-469537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New nucleic acid encoding EPH-like and related vectors, host cells, pr diagnostically and therapeutically
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-FEB-1999 (first entry)
Rat receptor tyrosine kinase Ehk-2.
Receptor tyrosine kinase; Ror-1; Ror-2; Ehk-1; Ehk-2; neurotrophin activity; trkB; proto-oncogene; tyrosine binding protein; BDNF; NT-3; diagnosis.
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Claim 18; Page 62-65; 133pp; English.
       proteins
Example;
                                                                                                                                                       Maisonpierre PC, Masiakowski WPI; 99-044584/04.
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Fox GM, Jing S, Welcher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R85091 standard; Protein; R85091;
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L5-APR-1994; US-229509.
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kinase receptor;
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Best Local Similarity 59...
Matches 13; Conservative
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Embryonic stem cell kinase (Esk).
Embryonic stem cell kinase; receptor
epithelium; signal transduction; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes nucleic acid molecules for ror-1, ror-2, ehk-1 and ehk-2. Also described are the corresponding prot Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor tyrosine kinases. The present sequence represents rat Ehk-2. Sequence 948 AA;
                misc_difference
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192
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205
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387
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312
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107
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278
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331. .4
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59.1%;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                  PT DNA encoding embryonic stem cell kinase, receptor tyrosine kinase - production of modulators and antibodies, useful to treat mucositis and other disorders involving epithelium Claim ; page 48-54; 98pp; English.

Novel mouse embryonic stem cell kinase (Esk) is a receptor tyrosine kinase that belongs to the Eph subfamily. Its amino acid sequence was deduced from a DNA molecule (T72320) isolated from a murine liver cDNA library. Recombinant Esk polypeptides, esp. soluble Esk (extracellular domain), can be produced in host cells and used for ligand isolation, as antagonists of Esk-ligand interaction and as immunogens for prodn. of antibodies useful as diagnostic reagents or therapeutic antagonists of Modulation of Esk expression can be used to treat mucositis (partic. when caused by cancer treatment), and as Esk is expressed in all epithelial tissues its modulation may be used to treat e.g. skin injuries, hair loss, corneal or peptic ulcers, ulcerative colitis, oesophageal reflex, sjorgren's syndrome and related autoimmune disease, mucosal infections and pancreatitis.
                                                                                                                                                                                                                                                                               Matches
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Best Local :
R85092 standard; Protein; 998
R85092;
16-APR-1996 (first entry)
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03-JUL-1997.
20-DEC-1996; AU0826.
22-DEC-1995; AU-007277
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11; Conserv
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339
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60
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415
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ATP binding motif"
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657
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/note= "characteristic of Eph subfamily"
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/note= "characteristic of Eph subfamily"
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57.9%;
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    Glycosylation
    "potential N-linked

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"potential N-linked
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"GXGXXG ATP binding motif"
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0.11;
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Best Local
11 JUL 1996.
03 JAN 1996; U00419.
03 JAN 1995; US-368776.
(PLAC ) MAX PLANCK GES FC
(SUGE-) SUGEN INC.
Clossek T. Millauer B,
WPI: 96-333988/33.
N-PSDB; T32961.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 Novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7 HEK8 and HEK11 (R85089-92), respectively, were identified following isolation of their encoding cDNAs (T02946-49) from a human foetal brodNA library. HEK5, HEK7 and HEK8 show extensive homology to the catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8. HEK11 shows no homology to any known EPH-like receptor. Recombinant HEK receptors (or their soluble extracellular domains) are produced expression of encoding sequences in procaryotic or eucaryotic host cells, and are used to produce antibodies (utilised in diagnostic assays), or to identify and purify ligands for HEK receptors, or therapeutically to modulate the activation of cell-associated
                                                                                                                                                                                                                                                                                                                         Mouse developmental kinase 1 MDK1 T1.

Mouse developmental kinase 1; MDK1 T1; receptor tyrosine kinase;

RTK; signal transduction; probe; diagnosis; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding EPH-like receptor tyrosine kinase(s) and related vectors, host cells, proteins, antibodies etc., used diagnostically and therapeutically to modulate receptor activation
                                                                                                                                                                                                                                                                                                                                                                                             W03422
                                                                                                           WO9621013-A1.
                                                                                                                                     misc_difference
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14-APR-1995; U04681.
15-APR-1994; US-229509.
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WO9528484-A1.
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EPH-like receptor protein tyrosine kinase; PTK; HEK11;
human eph-like kinase; therapy; diagnosis; antibody; vector
                                                                                                                                                                                                                                                                                                 Mus sp.
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95-373799/48.
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343. 345
/label= N-glycosylation_site
410. 412
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64. .66
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                                                       FOERDERUNG
                                                                                                                       "product of alternative splicing"
                                                                                                                                                  Transmembrane_domain
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Best Local Similarity
Matches 14; Conserv
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CDNA cloning using adult mouse brains and Northern blotting identified 2 truncated versions, MDKI T1 (W03422) and MDKI T2 (W03423), of the novel mouse developmental kinase 1 (MDKI) (see also W03421), a new member of the eck/eph family of receptor tyrosine kinases. Their amino acid sequences were deduced from cDNA clones (T32961 and T32962) obtd. from adult mouse brains. MDK T1 and T2 each possess the entire ectodomain, the transmembrane domain and part of the juxtamembrane region of MDK1, but lack the catalytic tyrosine kinase domain. They can be used to screen for potential agents useful for treatment of diseases characterised by abnormal signal transduction.

Sequence 610 AA;
Example 1; Page 113-115; 128pp; English.

CDNA cloning using adult mouse brains and Northern blotting using adult mouse brains and Northern blotting identified 2 truncated versions, MDKI T1 (W03422) and MDKI T2 (W03423), of the novel mouse developmental kinase 1 (kDKI) (see also W03421), a new member of the eck/eph family of receptor tyrosine kinases. Their amino acid sequences were deduced from cDNA clones (T32961 and T32962) obtd. from adult mouse brains. MDK T1 and T2 part of the juxtamembrane region of MDKI, but lack the catalytic tyrosine kinase domain. They can be used to screen for potential agents useful for treatment of diseases characterised by abnormal
                                                                                                                                                                          New mouse development kinase 1 gene - used for developing prods. diagnosis and treatment of abnormalities in signal transduction pathways
                                                                                                                                                                                                                                           11-JUL-1996.
03-JAN-1996; U00419.
03-JAN-1995; US-368776.
03-JAN-1995; US-368776.
(PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN (SUGE) SUGEN INC.
C10s9ek T, Millauer B, Ullrich A;
WPI; 96-339988/33.
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Mouse developmental kinase 1; MDK1 T2; receptor tyrosine kinase;
RTK; signal transduction; probe; diagnosis; gene therapy;
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                                                                                              Example 1; Page 105-108; 128pp; English.

SExample 1; Page 105-108; 128pp; English.

Concluse developmental kinase 1 (MDK1) (W03421) is a new member of the ceck/eph family of receptor tyrosine kinases (RTKs). Its amino call sequence was deduced from a cDMA clone (T32960) isolated from mouse embryo and adult brain libraries. The distinct patterns of MDK1 expression during mouse development suggest an comportant role for MDK1 in the formation of neuronal structures. Composition of the diagnosis of diseases characterised by abnormality in a signal transduction pathway, such as neuroproliferative or neurodegenerative disorders or cancer, to screen for (ant)agonists, and to raise antibodies.
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03-JAN-1996; U00419.

03-JAN-1995; US-368776.

(PLAC) MAX PLANCK GES F.

(SUGE-) SUGEN INC.

Clossek T. Millauer B.
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WPI; 96-
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Key
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Mouse developmental kinase 1.
Mouse developmental kinase 1; MDK1; receptor tyrosine kinase;
signal transduction; probe; diagnosis; therapy;
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RESULT W19968 ID W1

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W19968

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DR N-PSDB; 771086.

PT Imman and yeast alanyl-tRNA synthetase genes - useful for production of recombinant enzymes for diagnostic and analytical applications PS Claim 3; Column 43-48; A2p; English.

CC W19968 shows the amino acid sequence of human alanyl-tRNA synthetase CC (Ala-tRS). Human Ala-tRS and antibodies specific for it, may be useful CC in assays for diagnosing and monitoring an autoimmune disease known as CC antisynthetase syndrome. A condition in which patients having CC polymyositis and/or dermatomyositis produce antibodies against the cessential synthetase enzyme. Anti-synthetase syndrome is characterised by a number of clinical presentations, including interstitial lung CC disease, arthritis, Raynaud's phenomenon and fever. Human Ala-tRS can CC on human Ala-tRS. Tester strains comprising host cells containing CC function of the native gene which complements or substitutes the CC function of the native gene can be used to test for any toxic effects of such antimicrobial agents that specifically interacts with the human CC Ala-tRS gene or protein. Ala-tRS proteins can be used to separate CC alanine from other amino acids, to separate L-alanine from D-alanine, CC Guantitative determination of alanine or Aff.
                                                                                                                                                                        Query Match 47.1
Best Local Similarity 47.1
Matches 10; Conservative
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21-APR-1995; 426236.
21-APR-1995; US-426236.
(CANC-) CANCER INST JAPANESE FOUND CANCER.
(CUBI-) CUBIST PHARM INC.
(MASI ) MASSACHUSETTS INST TECHNOLOGY.
Ripmaster TL, Schimmel PR, Shiba K;
WPI; 97-280271/25.
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Human alanyl-tRNA synthetase.
Alanyl-tRNA synthetase; ligase; analysis; diagnosis; autoimmune;
disease; antisynthetase syndrome; interstitial lung disease;
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19-AUG-1997
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399 SLGDSKTIPGDTAWLLYDTYG 419
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9: sp_bage:*
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12: sp_virus:
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09y0y9 drosophila
09z330 rattus ratt
094559 schizosacch
018215 caenorhabdi
088893 tobacco rin
081339 mesembryant
019445 caenorhabdi
P73491 synechocyst
P91851 caenorhabdi
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Q76154 dugesia jap
081224 arabidopsis
081225 arabidopsis
080462 arabidopsis
Q80462 arabidopsis
Q23683 caenorhabdi
Q9wtx3 rattus norv
002232 caenorhabdi
Q27520 methanobact
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075851	Q92072	017237	Q9YHD9	P96418	081887	Q9ZQR4	Q15885	Q9Z6F5	Q9XBS0	017231	085538	P87266	Q66939	Q62338	Q9Z918	Q13816	092364	Q96891	Q68534	P79922	Q66960	Q58373	P79333	Q9X958
075851 homo sapien	N	017237 caenorhabdi	Q9yhd9 brachydanio	P96418 mycobacteri	O81887 arabidopsis	Q9zqr4 arabidopsis		Q9z6f5 vibrio para		017231 caenorhabdi	Q85538 feline immu	P87266 saccharomyc	Q66939 feline immu	8 mus muscu	chlam	Q13816 homo sapien	hog		hog chol	P79922 xenopus lae	Q66960 feline immu		P79333 oryctolagus	Q9x958 streptomyce

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REDIEN
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Best Local Similarity
Matches 16; Conser
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017572;
01-NOV-1996 (TIEMBLIZE1. 0
01-NOV-1996 (TIEMBLIZE1. 0
01-JAN-1999 (TIEMBLIZE1. 0
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C01G6.3.
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Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rhal
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105 IDFQMRLLILLICSAFSTCSVLDSFRANGIEFEVYGEGRLIPE
                                                  .3 PROTEIN
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Rhabditidae; Peloderinae; Caenorhabditis
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                              Score 58.5;
Pred. No. 0.
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RESULT
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Best Local
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OGATA S., WATANABE K.;

Planarian Na+/K+ ATPase alpha-subunit.";

submitted (MAR-1998) to the EMBL/GenBank/DDBJ dat

EMBL; AB012391; BAA32798.1; .

PFAM; PF00112; E1-E2_ATPase; 1.

PFAM; PF00689; Na_K_ATPase_C; 1.

PFAM; PF00689; Na_K_ATPase_N; 1.

PFAM; PF00690; Na_K_ATPASE.

PRINTS; PR00111; CATATPASE.

PRINTS; PR00121; NAKATPASE.

PRINTS; PR00121; NAKATPASE.

PRINTS; PR00121; NAKATPASE.
                                                                                           Matches
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O76154;
O76154;
O1-NOV-1998 (Tremblrel. 08, La
O1-NOV-1999 (Tremblrel. 12, La
NA+/K+-ATPASE ALPHA-SUBUNIT.
DJNAK.
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euphyllophytes;
core eudicots; R
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081224;
01-NOV-1998
01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                                      LEE Y.-R.J., ASSMANN S.M.;

"Arabidopsis thaliana extra-large G-protein: a new class binding protein.";

Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF066941; AAC19352.1; -.

HSSP; P10824; 1BH2.

PFAM; PF00503; G-alpha; 1.
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-CV. COLUMBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophy euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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Eukaryota; Metazoa; Platyhelminthes;
Paludicola; Dugesiidae; Dugesia.
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    116
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DCELSSSGELLLRSCSVKESLDLNESSSNPLVPDWESNE
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7; Conserv
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AA; 98796 MW;
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12,
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Last sequence update)
Last annotation update)
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Last sequence up
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Pred. No. 23;
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STRAIN-CV. KAUL S., LIN X., KETC
ROUNGLEY S.D., KAUL S., LIN X., KETC
HARNDON R.C., SYKES S.M., MASON T.M.
SOMERVILLE C.R., VENTER J.C.;
T "Arabidopsis thaliana chromosome II
L submitted (JUN-1998) to the EMBL/Ge
L Submitted (JUN-1998) to the EMBL/Ge
EMBL, AC003040; AAC23761.1; -
JR HSSP; P10824; 1AS2.
JR HSSP; P10824; 1AS2.
JR HSSP; P10824; 1AS2.
JR FFAM; PF00503; G-alpha; 1.
JR FFAM; PF00503; G-alpha; 1.
JR FFAM; PF00503; G-alpha; 1.
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Best Local S
Matches 17
                                                                                                  Query Match
Best Local S
Matches 17
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O81225;
O1-NOV-1998 (TrEMBLTel. (
O1-NOV-1998 (TrEMBLTel. (
O1-NOV-1999 (TrEMBLTel. )
EXTRA-LARGE G-PROTEIN.
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01-NOV-1998
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LIEE Y.-R.J., ASSMANN S.M.;
"Arabidopsis thaliana extra-large G-protein: a new class binding protein.";
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF660942; ARC19353.1; -.
HSSP; P10824; 1BH2.
PFAM; PF00503; G-alpha; 1.
SEQUENCE 888 AA; 98860 MW; 3F6B542C CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
01-NOV-1999 (TrEMBLRel. 12, Last annotation update)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;

core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
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DCELSSSGELLLRSCSVKESLDLNESSSNPLVPDWESNE
                             DCQLSI---LLLLSCSVLDSF------GELIPQ-PSNE
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17; Conserv
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nilarity 43.6%;
Conservative
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EMBL/GenBank/DDBJ
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Last sequence update)
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Pred. No. 23;
3; Mismatches
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                                                                                                                                                    901;
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                                                                                               Gaps
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Best Local S
Matches 9
DENG J., SZYF M.;
Submitted (AUG-1998) to the EL
EMBL; AF083043; AADZ8102.1; -
EMBL; AF083038; AADZ8102.1; J.
EMBL; AF083039; AADZ8102.1; J.
EMBL; AF083041; AADZ8102.1; J.
EMBL; AF083041; AADZ8102.1; J.
                                                                                                                                                           MEDLINE; 98389/UJ.

DENG J., SZYF M.;

"Multiple isoforms of DNA methyltransferase are

"wartebrate cytosine DNA methyltransferase gene."

Piol. Chem. 273:22869-22872(1998).
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BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULS
CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN
PARSONS J., PERCY C., RIFKEN L., ROPRA A., SAUNDERS D., SHOWNK
SMALDON N., SMITH A., SONNHAMMER B., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
"2.2 Mb of contiguous nucleotide sequence from chromosome III o:
elegans.";
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01-JAN-1996
01-JAN-1999
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Q23683;
                                                                                                                                  DENG J., SZYF M.;
                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
CYTOSINE DNA METHYLTRANSFERASE (FRAGMENT).
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Eukaryota; Metazoa; Nemat
Rhabditina; Rhabditoidea;
                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                          Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9WTX3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9WTX3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 368:32-38(1994).
EMBL; Z49073; CAA88891.1;
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CRLAILALFSVAMVSVYGQDTPPP
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9; Conser
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94150718.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata;
Sciurognathi; Muridae; Murinae;
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bidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Last sequence up
Last annotation
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                                                                                                              EMBL/GenBank/DDBJ
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on update)
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Rattus.
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Best Local S
Matches 8
                                                                                            027520
027520;
01-JAN-1998
01-JAN-1998
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 368:32-3
EMBL; Z83102; C
SEQUENCE 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WATSON A., "2.2 Mb of elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1997
01-JAN-1998
01-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON
CRAXTON M., DEAR S., DU Z., DUBIN R., FAVELLO A., FULTON L.,
GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L
JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
LIGHTNING J., LLOYD C., MCMURRAY A., MORTINORE B., O'CALLAGHAN M.
PARSONS J., PERCY C., RIFKEN L., ROOPAA A., SUNDERS D., SHOWNKEE
SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
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WILSON R., AINSCOUGH
BONFIELD J., BURTON C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF083042; AAD28102.1; JOINED Transferase; Methyltransferase. NON_TER 1 1 NON_TER 349 349 SEQUENCE 349 AA; 39021 MW; CCB:
                                   Methanobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caenorhabditis elegans.
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C54C8.4.
Methanobacterium
              Archaea;
                                                                            TRYPTOPHAN
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rocal Similarity
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283102; CAB05466.1;
ICE 399 AA; 46244
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8; Conservative
                Euryarchaeota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (NOV-1996)
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8 (TrEMBLrel. 05, Last seq
9 (TrEMBLrel. 12, Last ann
SYNTHASE, BETA SUBUNIT HO
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39021 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nematoda; Secernentea; Rhabditia; Rhabditida;
bidea; Rhabditidae; Peloderinae; Caenorhabditi
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09,
              Methanobacteriales;
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                                                                                                                                                                                                                                                                                                                                                            Score 47; DB Pred. No. 25; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL/GenBank/DDBJ databases
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                                                                         HOMOLOG.
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              Methanobacteriaceae;
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STRAIN=CV. COLUMBIA;
VYSOTSKAIA V.S., SCHWARTZ J.R., TORIUMI M., YU G.,
KREMENETSKAIA I., LUROS J., ARAUJO R., BUEHLER E.,
DEWER K., FENG J., KIM CV., LI Y., SHINN P., SUN H.,
BCKER J.R., FEDERSPIEL N.A., THEOLOGIS A.;
"Arabidopsis thaliana chromosome 1 BAC F15K9 sequer
"Arabidopsis thaliana chromosome 1 BAC F15K9 sequer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMITH D.R., DOUCETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DUBOIS ALDREDGE T., BASHIZADEH R., BLAKELY D., COOK R., GILBERT K., HARRISON D., HOANG L., KEAGLE P., LUMM W., POTHIER B., QIU D., SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R., JUWANI N., CARUSO A., BUSH D., SAPER H., PATWELL D., PRABHAKAR S., MCDOUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M., DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.; DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.; "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155(1997).
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SEQUENCE FROM
STRAIN-DELTA
  MENDEL; 3
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; eudicotyledons;
euphyllophytes; Rosidae; eurosids II; Brassicales; Brassicaceae;
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F15K9.13.
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01-NOV-1999
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                                                                                                               SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
                                                                                                                                                                                   Submitted
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tted (NOV-1998) to the EMBL/GenBan)
AC005278; AAC72127.1; -
LL; 38431; Arath;3293;38431.
NCE 514 AA; 56415 MW; B6C24CB4
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429 AA; 47487 MW;
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Last sequence up
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                                                                                                                                                                              EMBL/GenBank/DDBJ databases
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Matches
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RUBIN G.M., WAN K.H., HARVEY D., LEWIS S.E., BROKSTEIN P., TSANG G., AGBAYANI A., ARCAINA T.T., BAXTER E., BLAZEJ R.G., BUTENHOFF C., CHAWPE M., CHAVEZ C., CHEW M., DOYLE C.M., FARFAN D.E., FRISE E., GALLE R., GEDRGE R.A., HARRIS N.L., HOSKINS R.A., EVANS-HOLM M., HOUSTON K.A., HUMMASTI S.R., KIM E., J., MOSHREFI M., PACLEB J.M., PARK S., SEQUEIRA A., SETHI H., SNIR E., SVIRSKAS R.R., WEINBURG T., CELNIKER S.E.;

"Full length Drosophila melanogaster cDNA sequence.";

"Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

EMBL: AF145687; AAD38662.1; -.

EMBL: AF145687; AAD38662.1; -.

SEQUENCE 1146 AA; 124541 MW; 8DA1D02B CRC32;
                                                                                                                                                             "Expression of rat DNA (cytosine-5) methylt rodent trophoblast giant cells: molecular c of rat DNA MTase.";
Biochem. Bionhma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9Y0Y9
                   Biochem. Biophys. Res. Commun. 253:495-501(1998).
-!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + I
ADENOSYL-L-HOMOCYSTEINE + DNA 5-METHYLCYTOSINE.
-!- SIMILARITY: STRONG, TO OTHER C5-DNA METHYLASES.
EMBL; AB012214; BAA37118 1;
-PROSITE; PS00094; C5_MTASE_1; 1.

PROSITE; PS00095; C5_MTASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                            Rattus rattus (black rat).
Eukaryota; Metazoa; Chorda
Eutheria; Rodentia; Sciuro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1999 (TIEMBLIFE! 10, Created)
01-MAY-1999 (TIEMBLIFE! 10, Last sequence update)
01-NOY-1999 (TIEMBLIFE! 12, Last annotation update)
MODIFICATION METHYLASE (EC 2.1.1.73) (CYTOSINE-SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9Z330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BCDNA.LD24702.
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TISSUE-BRAIN, AND PLACENTA;
MEDLINE; 99097263.
KIMURA H., TAKEDA T., TANAK
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    Transferase;
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    Methyltransferase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 47; DB Pred. No. 69; 1; Mismatches
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  Restriction system
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methyltransferase
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01-JAN-1998 (TIEMBLIEL (
01-NOV-1999 (TIEMBLIEL )
1753C12B 1 PROTEIN.
Y53C12B 1.
  SEQUENCE FROM N.A.
MEDLINE; 94150718.
WILSON R., AINSCOUGH R.,
BONFIELD J., BURTON J., C
CRAXTON M., DEAR S., DU Z
GARDNER A., GREEN P., HAW
                                                           Submitted ([2]
                                                                                                        Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditina; Rhabditoidea; Rha
                                                                                                                                                                                       018215;
018215;
                                                                                                                                                                                                                                                                                                                                  STRAIN-972H-;
BARRELL B.G., RAJANDREAM M.A., WOOD V.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ
EMBL; 299753; CAB16876.1; -.
Hypothetical protein.
SEQUENCE 431 AA; 49532 MW; 67F4D4CF CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Archiascomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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STRAIN-972H-;
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01-MAY-1999 (TrEMBLrel.
HYPOTHETICAL 49.5 KD PRC
SPAC23C4.05C.
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Submitted (OCT-1997) to
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J., LENNARD N.;
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R., ANDERSON K., BAYNES C., BERKS M.,
CONNELL M., COPSEY T., COOPER J.,
CONTELL M., FORTON
COPSEY T., COOPER J.,
COPSEY T., COOPER J.,
COPSEY T., BAYELLO A., FULTON
HAWKINS T., HILLIER L., JIER M., JOH
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A LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAI
A PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWI
A SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
A THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON J.
A WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
T "2.2 Mb of contiguous nucleotide sequence from chromosome III
T elegans.";
L Nature 368:32-38(1994).
R REMBL; 279278; CAB16490.1; -.
R PFAM; PF00400; WD40; 6.
R PFAM; PR00320; GPROTEINBRET.
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Q88893;
01-NOV-1996
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EMBL; U50869; AAB03785 1; -.
PFAM; PF00680; RNA_dep_RNA_pol; 1.
PFAM; PF00910; RNA_helicase; 1.
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ZALLOUA P.A., BUZAYAN J.M., BRUI "Chemical cleavage of 5'-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-BUD BLIGHT; MEDLINE; 96204566.
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Tobacco ringspot virus (Tobrsv) (Trsv).
Viruses, ssRNA positive-strand viruses,
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       2000, 22:32:08; Search time 49.21 Seconds (without alignments) 17.947 Million cell updates/sec
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     EPA3 HUMAN
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Y091 PVACE
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Y091 PVACE
EPA3 CHICK,
MIDM MOUSE
INAL JIG
INAL JIG
INAL YEAST
PSPB RABIT
DPOL ARCFU
SYFB SYNY3
MGR8 HUMAN
FIBG XENLA
ATHL HUMAN
CALT BOVIN
PTRR DIDMA
LYST HUMAN
CPV1 BRARE
YFBK ECOLI
RRP2 IAGUZ
NULM ARBLI
INAL BOVIN
INAE BOVIN
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008680 rattus norv
p51942 mus musculu
p41479 autograph
     P13864
P49879
P09838
P138913
P138913
P14296
P074296
P07634
P54707
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P251033
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5 oryctolagus
3 archaeoglob
6 synechocyst
2 homo sapien
4 xenopus lae
7 homo sapien
3 bos taurus
7 didelphis m
8 homo sapien
5 brachydanio
1 escherichia
7 influenza a
6 arbacia lix
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8 gallus gall
4 mus musculu
9 sus scrofa
8 mus musculu
3 saccharomyc
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EMBL; M83941; AAA58633.1; -.
EMBL; AA8003; CAA01906.1; -.
PII; A38224; A38224.
HSSP; P00523; 2PTK.
MIM; 179611; -.
PRLWTS; PR00104; FNTYPEIII.
PRLWTS; PR00109; TYRKINASE.
PRINTS; PR00109; PROTEIN_KINASE_ATP; 1
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1
PROSITE; PS0011; PROTEIN_KINASE_DOM; 1

PATT P2355 PYEAST P43548 FIVEZ PATT P43548 FIVEZ PATT P43548 P47743 P4774 P47743 P4774 P477	
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P22355 P22355 P22355 P23548 Q04348 Q04346 Q04046 Q060466 Q060466 Q060466 Q060466 Q060466 Q060466 Q060466 Q07TROSINE-F Q07TROSINE-F Q07TROSINE-F Q07TROSINE-F Q07TROSINE-F Q07TROSINE-F Q07TROSINE-F Q0601885 Q06046 Q0601885 Q060468 Q0601885 Q060468 Q07TROSINE-F Q0601885 Q060468 Q0601885 Q060468 Q0601885 Q060468 Q07TROSINE-F Q0601885 Q060468 Q0601885 Q060468 Q	
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RESULT 2
EPA3_MOUSE
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           RC STRAIN-ICR X SWISS WEBSTER; TISSUE-EMBRYO;

RX MEDLINE; 92031278.

RX MEDLINE; 9203128.

RX 
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Best Local
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RP_BIND

BINDING

BINDING

ACT_SITE

MOD_RES

CARBOHYD

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CONFLICT

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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.1112)
KINASE RECEPTOR ETK1) (MEK4).
EPHA3 OR ETK1 OR MEK4 OR TYRO4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Eukaryota; M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; PS031186; EGF_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MDCQLSILLLSCSVLDSFGELIPQPSNE 29
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PF00069; pkinase; 1.
PF00536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF01404;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Mouse).
etazoa; Chordata; Craniata; Vertebrata; Mammalia;
יאביילוא: Sciuroqnathi; Muridae; Murinae; Mus.
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110086 MW;
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Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
POTENTIAL.
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FIBRONECTIN TYPE-III.
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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Pred. No. 3
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-> L (IN CAA01906).
B8D900FA80FF5121 CRC64;
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Best Local S
Matches 21
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PRINTS; PRO0109; TYRKINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00791; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00799; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00799; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00793; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PFAM; PF00041; fn3; 2.

PFAM; PF00069; pkinase; 1.

PFAM; PF00069; pkinase; 1.

PFAM; PF00069; SAM; 1.

PFAM; PF001404; EPH_lbd; 1.
               008680;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation updat
EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.
KINASE RECEPTOR REK4).
                                                                                                                                                                                                                                                                                        ACT_SITE
MOD_RES
CARBOHYD
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TRANSMEM
DOMAIN
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BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M68513; AAA39521.1; -.
EMBL; M68515; AAA39522.1; ALT_SEQ.
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-i- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
              EPHA3 OR REK4
                                                                                                   EPA3_RAT
                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
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HSSP; P16109; 1FSB.
 Rattus
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                                                                                                                                                                щ
                                                                                                                                                                                      1 MDCQLSILLLSCSVLDSFGELIPQPSNE 29
                                                                                                                                                              MDCHLSILVLLGCCVLSCSGELSPQPSNE
norvegicus (Rat)
                                                                                                                                                                                                             h 71.4%;
Similarity 72.4%;
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane;
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                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                          109955
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BY SIMILA
                                                                                                                                                                                                                                                                             W.
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                                                                                                                                                                                                             Score 105; DB Pred. No. 7.1e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                              ATP (BY SIMIL)
ATP (BY SIMIL)
BY SIMILARITY
                                                                                                                                                                                                                                                                                      PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                 FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III. PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYS-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPHRIN TYPE-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kinase; ATP-binding; Phosphorylation; oprotein; Signal; Alternative splicing BY SIMILARITY.
                                                                                                 PRT;
                                                                                                                                                                                                                                                                            BE44A6655D8107A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY). (BY SIMILARITY).
                                                                                                                                                              29
                                                                                                 984
                                update)
| 2.7.1.112) (TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                 ₿
                                                                                                                                                                                                                            , 1e-08;
                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RECEPTOR 3
                                                                                                                                                                                                                                     Length 983;
                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    restrictions
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PROSITE; PS00109; PROTEIN_KINASE_TYR;
PROSITE; PS00111; PROTEIN_KINASE_DOM;
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PFAM; PF00041; fn3; 2.
                                                                                                                                                               MOD_RES
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NP_BIND
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "IL1 Y. Y., MCTIernan C.F., Feldman A.M.;
"IL1 beta alters the expression of the receptor r-EphAs in neonatal rat cardiomyccytes.";
Am. J. Physiol. 274:H331-H341(1998).
-I. FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-EPHRIN-A2, -A3, -A4 AND -A5.
-I. CATALYTIC ACTIVITY: AIP + A PROTEIN TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U69278; AAC06273.1; -
HSSP; P16109; 1FSB.
PRINTS; PR00014; FNTYPEIII.
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00069; pkinase; 1. PFAM; PF00536; SAM; 1. PFAM; PF01404; EPH_lbd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase; Tyrosine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ÷
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE; 98120505.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE FINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                    MDCQLSILLLLSCSVLDSFGELIPQPSNE
MDCHLSILILFGCCVLSCSRELSPQPSNE
                                                                                       Similarity
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                                                                        Conservative
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PROTEIN_KINASE_TYR;
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RECEPTOR_TYR_KIN_V_1;
RECEPTOR_TYR_KIN_V_2;
                                                                                                                                                                                                  63.9%;
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BY SIMILARITY.
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Pred.
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POTENTIAL.
v; F170C49312F7A0AB CRC64;
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BY SIMILARITY).

PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

POTENTIAL.

POTENTIAL.

POTENTIAL.
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CYS-RICH.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
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                                                                                                                                                                                                                                                                                                                                                PROTEIN KINASE
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                                                                      Mismatches
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RESULT 5
Y091_NPVAC
ID Y091_N
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SEQUENCE
Y091_NPVAC STANDARD;
P41479;
01-NOV-1995 (Rel. 32, Created)
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CHAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning, sequencing and expres matrix protein cDNA.";
Eur. J. Biochem. 236:970-977(19
-1- FUNCTION: CARTILAGE MATRIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARTILAGE MATRIX PROTEIN PRECURSOR MATN1 OR CRIM OR CMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
15-DEC-1998 (Rel. 37, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P51942;
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:106591; MATN1.
PRINTS; PR00453; VWFADOMAIN.
PROSITE; PS00022; EGF_1; FAI
PROSITE; PS01186; EGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U35035;
HSSP; P05099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Eutheria; Rodentia; Sciurogna;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAMA_MOUSE
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MEDLINE; 96270751.
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                                                                                                                                                12
                                                                                                                                                                                  3 CQLSILLLLSCSVLDSFGELIPQP
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268 457
268 457
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                                                                                                                                                                                                                                                                                                                                 54446
                                                                                                                                                                                                                                               35.7%;
54.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-CARTILAGE;
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Pred. No. 2
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5746028F7E11EFA6 CRC64;
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Mus.
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Hypothetical protein.
SEQUENCE 224 AA
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01-NOY-1997 (Rel. 35, Last annotation update)
HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P3 INTERGENIC REGION.
Autographa californica nuclear polyhedrosis virus (AcmnPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1997 (Rel. 35, Last annotation update)
01-NOY-1997 (Rel. 35, Last annotation update)
EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ETK1) (CEK4).
EPHA3 OR ETK1 OR CEK4
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                              from mouse and chicken that is deve
at least two forms of the receptor.
New Biol. 3:769-778(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                Sajjadi F.G., Pasquale E.B., Subramani S., "Identification of a new eph-related receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 92031278.
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                                                                                                - ! - SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16
                                                                                                                                                                                              FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A
EPHRIN-A2, -A3, -A4 AND -A5.
CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE =
PROTEIN TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: GREATEST LEVELS OF EXPRESSI
                                                                                                                         SIMILARITY: TO COMMIN. BELONGS
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                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBI outstation -
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10; Conservative
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; Galliformes; Phasianidae; Phasianinae; (
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Bioinformatics
                                             TO OTHER PROTEIN .....ONGS TO THE EPHRIN RECEPTOR FAMILY.
CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
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the EMBL outstation - restrictions on its
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Matches 11
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PRINTS; PRO0109; TYRKINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TOW; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PFAM; PF00041; fn3; 2.

PFAM; PF00069; PkInase; 1.

PFAM; PF00053; SAM; 1.

PFAM; PF01404; EPH_1bd; 1.
                                                                                                                                                                                                                                                        P13864;
01-CAN-1990 (Rel. 13, Created)
01-NOY-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, Last annotation update)
DNA (CYTOSINE-5)-METHYLTRANSFERASE (EC 2.1.1.37)
DNA (CYTOSINE-5)-METHYLTRANSFERASE (MCMT) (M.MMUI).
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SEQUENCE
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ACT_SITE
MOD_RES
Bestor T.H., Laudano A., Mattaliano R., Ingram V.; "Cloning and sequencing of a cDNA encoding DNA methyltransi mouse cells. The carboxyl-terminal domain of the mammalian related to bacterial restriction methyltransferases."; J. Mol. Biol. 203:971-983(1988).
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SIGNAL 1 19 BY SIMILARITY.
                                                                                                              SEQUENCE FROM N.A. MEDLINE; 89094873.
                                                                                                                                                                                                                            Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                               MIDM_MOUSE
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an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                Chordata; Craniata; Vertebrata;
Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                     Chordata;
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); E8895F0BDF77651E CRC64;
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PIR; S01845; S01845;
REBASE; RB02813; M.MmuI.
MGD; MGI:94912; Dnmt.
PRINTS; PR00105; CSMETTRFRASE.
PROSITE; PS00094; C5_MTASE_1; 1.
PROSITE; PS00095; C5_MTASE_2; 1.
PRAM; PF00145; DNA_Methylase; 3.
PRAM; PF011426; DNA_Methylase; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                INA1_PIG STANDARD; PRT; 189 AA. P49879; 01-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) INTERFERON ALPHA-1 PRECURSOR (IFN-ALPHA-1). Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
  SEQUENCE FROM N.A.
MEDLINE; 87035119.
Lefevre F., la Bonnardiere C.;
"Molecular cloning and sequencing of a
active porcine alpha-interferon.";
J. Interferon Res. 6.349-360(1986).
-!- FUNCTION: PRODUCED BY MACROPHAGES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -I- FUNCTION: METHYLATES CG RESIDUES.
-I- CATALTIC ACTIVITY: S-ADENOSYL-L-METHYLOYINE + DNA
-I- CATALTIC ACTIVITY: S-DENOSYL-L-METHYLCYTOSINE;
-I- SIMILARITY: HIGH, TO OTHER EURARYOTIC DNA METASE.
-I- SIMILARITY: SOME TO BACTERIAL RESTRICTION SYSTEMS
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Crar
Eukaryota; Metazoa; Chordata; Crar
                                                                                                                                                                                                                                                                                                 STRAIN-DOMESTICA;
MEDLINE; 92193689.
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J. Biol. Chem. 271:31092-31097(1996)
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REVISIONS TO N-TERMINUS.
MEDLINE; 97094871.
Yoder J.A., Yen R.C., Ve
                                                                                                                                                                                                                                analysis, and
                                                                                                                                                                                                                                                     Lefevre F., la Bonnardiere C.,
"The porcine family of interfe
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New 5' regions of the
                                                                                                                                                                                                        Interferon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DCNVLLKLVMAGEVTNSLGQRLPQ 1216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF01426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l Similarity
8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     651
1229
1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; BAH; 2.
6; BAH; 2.
Methyltransferase; DNA-binding.
Methyltransferase; DNA-binding.
651 CYS/ARG/LYS-RICH.
651 693 CYS/ARG/LYS-RICH.
1629 BY SIMILARITY.
1620 AA: 183286 MW; F737100AD043E709 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                   family of interferon-omega: functional studies of five Res. 11:341-350(1991).
                                                                                                                                                                                                                                                                                                                              TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.0%;
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e murine and h
MACROPHAGES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB
Pred. No. 51;
8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Mammalia;
                                                                                                                                                                                                                                                                            Mege
                                                                                                                                                                                                                                                                                                                                                                                                    Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human
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  IFN-ALPHA HAVE ANTIVIRAL
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                                                                                                                                                                                                                                                                                                                                                                                                       Sus.
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r DNA (cytosine-5)-
                                                                                                                                                                                                                           genes.";
                                                                                                                                                                                                                                                     structural
                                                                      biologically
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REAL SECTION OF SECTIO
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P09838;
01-MAR-1989 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                         Rougeon F., Doyen N.;
"The two isoforms of mouse differ in both the ability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Koiwai O., Yokota T., Kageyama T., Hirose T., "Isolation and characterization of bovine and deoxynucleotidyltransferase cDNAs expressible Nucleic Acids Res. 14:5777-5792(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-1989 (Rel. 10, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMINAL A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISULFID DISULFID
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SIGNAL
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EMBL; M28623; AAA31053.1;
HSSP; P01563; lITF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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the Euro
                                     differ in both the localization.";
                                                                                                                                             Bentolila L.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE; 86286588.
                                                                                                                                                                                CHARACTERIZATION C
MEDLINE; 96016194.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koiwai O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT
                               localization.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 LTALVLLSCNAICSLGCDLPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 LSILLLLSCSVLDSFGELIPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTIVITIES. INTERPERON STIMULATES THE PRODUCTION OF TWO A PROTEIN KINASE AND AN OLIGOADENVLATE SYNTHETASE. SIMILARITY: BELONGS TO THE INTERPERON ALPHA, BETA AND DEFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Electropean Bioinformatics Institute. There are no restricted the state of the s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      e; Antiviral; Multigene family; S
1 23 POTENTIAL.
24 189 INTERFEEND
D 24 122 BY SIMILARI
D 52 162 BY SIMILARI
E 189 AA; 21433 MW; 8C8BEA8DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 47.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Metazoa;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Mouse).
Metazoa; Chordata; Craniata; Vendentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                    Fanton
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                                                        terminal to add N
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BY SIMILARITY.
BY SIMILARITY.
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Pred. No.
                                                                                                                                             Υ.
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                                                                                                                                                Nguyen
                                                  deoxynucleotidyl transferase regions and subcellular
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7.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vertebrata;
ae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALPHA-1
                                                                                                                                          T.Q.,
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as its content
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                                                                                                                                                                                                                                                                                                                              Nguyen T.Q., Rougeon ates two forms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Yoshida S., Ara
d mouse terminal
e in mammalian ce
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                                                                                                                                                Martinez
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MBL outstation -
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RESULT 10
FADI_YEAST STANDARD; PRT; 306 AA.

ID FADI_YEAST STANDARD; PRT; 306 AA.

AC P38913;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE FAD SYNTHETASE (EC 2.7.7.2) (FMN ADENYLYLTRANSFERASE) (FAD PYROPHOSPHORYLASE) (FLAVIN ADENINE DINUCLEOTIDE SYNTHETASE).

GN FADI OR YDL045C OR DELOYIO (PAD PADI OR YDL045C OR PADI OR PADI OR YDL045C OR PADI O
RRR OCC GREET DATE
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Best Local S
Matches 10
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EMBL; X68670; CAA48634.1; -.
PIR; B23595; B23595.
MGD; MGI:98659; TDT.
PRINTS; PRO0869; DNAPOLX.
PRINTS; PRO0871; DNAPOLXTDT.
PROSITE; PS00522; DNA-POLYMERASE_X; 1.
PFAM; PF00533; BRCT; 1.
PFAM; PF00566; DNA-POLYMERASE_X; 1.
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -I- FUNCTION: TEMPLATE-INDEPENDENT DNA POLYMERASE WHICH CATALYZES THE RANDOM ADDITION OF DEOXYNUCLEOSIDE 5'-TRIPHOSPHATE TO THE 3'END OF A DNA INITIATOR. ONE OF THE IN-VIVO FUNCTION OF THIS ENZYME IS THE ADDITION OF NUCLEOTIDES AT THE JUNCTION OF THIS ENZYME IS THE ADDITION OF RUCLEOTIDES AT THE JUNCTION (N REGION) OF REARRANGED IG HEAVY CHAIN AND T CELLS.

-I- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE TRIPHOSPHATE + (DEOXY NUCLEOTIDE)(M) = N PYROPHOSPHATE + (DEOXYNUCLEOTIDE)(M+N).

-I- COFACTOR: REQUIRES MAGNESIUM.
-I- SUBCELLULAR LOCATION: NUCLEAR (TDT-S) OR CYTOPLASMIC (TDT-L).

-I- ALTERNATIVE PRODUCTS: TWO ISOFORMS; TDT-L/ARGE) (SHOWN HERE) AND IN ACTIVITY AS THE LONG CYTOPLASMIC FORM CAN NOT ACT ON N DEOXYNUCLEOTITY AS THE LONG CYTOPLASMIC FORM CAN NOT ACT ON N
                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetaceae; Saccharomyces.
STRAIN-W303-1A
MEDLINE; 95098
                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <del>-</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLLYCDILESTFEKFKQPSRK 394
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M -> T (IN REF. 1).
F -> L (IN REF. 1).
R -> G (IN REF. 1).
Q -> K (IN REF. 1).
E -> Q (IN REF. 1).
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23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 529;
                                                                                                                 Saccharomycetales
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EMBL; Z71781; CAA96444.1; -.
EMBL; Z71781; CAA9604.1; -.
PIR; S47906; S47906.
SGD; L0000598; FAD1.
SGD; L0000598; FAD1.
PFAM; PF01507; PAPS_reduct; 1.
Transferase; Nucleotidyltransferase; FASEQUENCE 306 AA; 35546 MW; 55BBB83C
                                                                                                                                                                      SEQUENCE ZEALL.
STRAIN-NEW ZEALL.
STRAIN-NEW ZEALL.
ROGGE
ROGGE
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
PULMONARY SURFACTANT-ASSOCIATED PROTEIN) (PULMONARY SURFACTANT-ASSOCIATED PROTEIN)
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Submitted (APR-1996) to the EMBL/GenBank/DDBJ da
-i- EUNCTION: ADENYLATES FMN TO FAD.
-i- CATALYTIC ACTIVITY: ATP + FMN - DIPHOSPHATE
                                                            "Transcription and mRNA stability regulate developmental and expression of rabbit surfactant protein B gene."; Am. J. Physiol. 268:L481-L490(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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                                                                                                                                                                                                                                                                                                                                                                            "Isolation and characterization associated protein-B (SP-B) in t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J., Richardson C.,
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                                                                                                                                                                  R.K., Boggaram V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                               G., Possmayer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 66.8; Conservative
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                                                                                                                                                                                                                                      ZEALAND WHITE;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spencer T.,
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15-JUL-1998
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DISULFID
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DISULFID
CARBOHYD
SEQUENCE FROM N.A. STRAIN-VC-16 / DSM MEDLINE; 98049343.
                                                                                                                                                    DPOL_ARCFU 029753;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                             DNA POLYMERASE (EC 2.7.7
POL OR POLB OR AF0497.
Archaeoglobus fulgidus.
Archaea; Euryarchaeota;
                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Surface
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Gene 165
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Luzi P., Anceschi M., Strayer D.S.;

"The upstream region of the SP-B gene: intrinsic promoter activity and glucocorticoid responsiveness related to a new DNA-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
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EMBL; U17116; AAA67934.1; -.
EMBL; S80649; AAD14335.1; -.
PIR; A32421; LNRBB.
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                                                                                                                                                                                                                                                     4 QLSILLLLSCSVLDSFGELIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: HOMODIMER, DISULFIDE-LINKED.
SUBCELLAULAR LOCATION: EXTRACELLULAR.
MISCELLANEOUS: PULMONARY SURFACTANT CONSISTS OF 90% LIPID AND 10%
PROTEIN. THERE ARE 4 SURFACTANT ASSOCIATED PROTEIN: 2 COLLAGENOUS,
CARBOHYDRATE-BINDING GLYCOPROTEINS (SP-A AND SP-D) AND 2 SMALL
HYDROPHOBIC PROTEINS (SP-B AND SP-C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; 165:285-290(1995).
FUNCTION: PULMONARY SURFACTANT ASSOCIATED PROTEINS PROMOTE
ALVEOLAR STABILITY BY LOWERING THE SURFACE TENSION AT THE AIR-
LIQUID INTERFACE IN THE PERIPHERAL AIR SPACES. SP-B INCREASES
THE COLLAPSE PRESSURE OF PALMITIC ACID TO NEARLY 70 MILLINEWTONS
                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                STANDARD;
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36, Last sequence update)
37, Last annotation updat
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                                                             Archaeoglobales;
           ATCC 49558
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B.
SAPOSINS-LIKE TYPE A.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
POTENTIAL.
MISSING (IN REF. 2).
R -> P (IN REF. 1).
C -> R (IN REF. 2).
ELHTPOLLSLLSRGWDARALGALGAC ->
AAHAPAAEPAYGGLGPRULPGPEGRV (IN REMAINS).
AAHAPAAEPAYGGLGPRULPGPEGRV (IN REMAINS).
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                                                           Archaeoglobaceae
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B_SYNY3
SYFB_SYNY3
P74296;
                                      Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S., "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).

-IT CATIVITY: ATP + L-PHENYLALANINE + TRNA(PHE) - AMP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artlach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (EC 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00136; DNA_DOL_B;
Transferase; DNA-directed
DNA-binding.
SEQUENCE 781 AA; 89850
                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 97061201.
                                                                                                                                                                                                                                                                                                               TRNA LIGASE BETA CHAIN) (PHERS).
PHET OR SLL1553.
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Nature 390:364-370(1997).
-I- CATALYTIC ACTIVITY: N DEOXYNUCLEOSIDE
                                                                                                                                                                                                                                                                                 Bacteria;
                                                                                                                                                                                                                                                                                                 Synechocystis
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PROSITE; PS00116; DNA_POLYMERASE_B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE001070; AAB90741.1; TIGR; AF0497; -.
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-!- SIMILARITY: BELONGS TO DNA POLYMERASE TYPE-B FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "The complete genome sequence of the hyperthermophilic, reducing archaeon Archaeoglobus fulgidus.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 MLVFDCEMLSSFG--MPEPEKD
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European Bioinformatics Institute. There are no restrictions on
by non-profit institutions as long as its content is in no
lifted and this statement is not removed. Usage by and for commen
                PYROPHOSPHATE + L-PHENYLALANYL-TRNA(PHE)
SUBUNIT: TETRAMER OF TWO ALPHA AND TWO B
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8; Conserv
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              TETRAMER
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Pred. No.
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48;
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              BETA
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Matches 12
EMBL; U92459; AAB517
EMBL; U95025; AAB720:
GCRDB; GCR_1889; -.
GCRDB; GCR_2604; -.
MIM; 601116; -.
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SEQUENCE FROM N.A.

MEDLINE; 97446143.

SCherer S.W., Soder S., Duvoisin R.M., Huizenga J.J., Tsui L.C.;

Scherer S.W., Soder S., Duvoisin R.M., Huizenga J.J., Tsui L.C.;

"The human metabotropic glutamate receptor 8 (GRM8) gene: a

disproportionately large gene located at 7q31.3-q32.1.";

Genomics 44:232-236(1997).

-i- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR

-i- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D90913; BAA18390.1; --
HSSP; P27002; 1PYS.
PFAM; PF01588; trNA_bind; 2.
Aminoacyl-trNA synthetase; P
SEQUENCE 810 AA; 87887 MW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wu S., Wright R.A., Rockey P.K., Burgett S.G., Arnold J.S., Rosteck P.R. Jr., Johnson B.G., Schoepp D.D., Belagaje R.M.; "Group III human metabotropic glutamate receptors 4, 7 and 8: molecular cloning, functional expression, and comparison of pharmacological properties in RGT cells."; Brain Res. Mol. Brain Res. 53:88-97(1998).
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Homo Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SIMILARITY: BELONGS TO
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                                                                                AAB51764.1; -.
AAB72040.1; -.
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FIBG_XENLA
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P17634;
01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence up
15-JUL-1999 (Rel. 38, Last annotation
FIBRINOGEN GAMMA CHAIN PRECURSOR.
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PRINTS; PR00598; MTABOTROPICR.
PRINTS; PR01058; MTABOTROPCBR.
PRINTS; PR001059; G_PROTEIN_RECEP_F3_1;
PROSITE; PS00980; G_PROTEIN_RECEP_F3_2;
PROSITE; PS00981; G_PROTEIN_RECEP_F3_3;
PROSITE; PS00991; G_PROTEIN_RECEP_F3_3;
PROMITE; PS00093; 7tm_3; 1.
                                                                                          "Estrogen regulation expression.";
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Eukaryota; Metazoa; Chordata; Cran
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                 MEDLINE;
                                 TISSUE=LIVER;
                                                SEQUENCE OF 1-58 FROM
                                                                               Biochemistry
                                                                                                                          Pastori R.L.,
                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                        Batrachia;
                                                                                                                                            (EDLINE;
                                                                                                                                                                                       enopus.
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90241882.
                 91146806
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Shepard A.R., Moser D.R., Holland L.J.;
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101741 MW;
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37
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                                                                                                          J.E., Sm
Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 45; DB Pred. No. 56; 7; Mismatches
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V (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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T -> I (IN REF. 2).
A -> G (IN REF. 2).
N -> I (IN REF. 2).
S -> T (IN REF. 2).
95C2D0886E743905 (
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lpoidea; Pipidae;
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.on update)
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                                                                                                          gamma-fibrinogen
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                                                                                                                                                                                                    Xenopodinae;
                                                                                                                                                                                                                      Amphibia
                                                                                                          gene
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Search completed: May Job time: 2402 sec
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Best Local S
Matches 11
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DISULFID
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AGGREGATION.

FISUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

(ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.

FISUBLE FOR SETSION OF FIBRINGEN TO FIBRIN IS TRIGGERED BY THROMBIN, WHICH CLEAVES FILBRINOPEPTIDES A AND B FROM ALPHA & BETA CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS CONVERTED INTO THE HARD CLOT BY FACTOR XILLA WHICH CATALYZES THE EPSILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS (CHENKE) AND SETWEEN AND 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P02679; 1FIC:
PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
PFAM; PF00147; fibrinogen_C; 1.
Blood_coagulation; Glycoprotein; Calcium; Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; J02894; AAA49709.1; -.
EMBL; M35548; AAA03247.1; -.
PIR; A32670; A32670.
HSSP; P02679; 1FIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOI. Celi. Endocrinol. 72:213-220(1990).
-i- FUNCTION: FIBRINGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Isolation of Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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9 LLLLQSLALLSSAFGNIIPNTDN 31
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                                                                                                                                                                                                                                                                                                         11; Conservative
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                               2000, 22:32:11
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INTERCHAIN (WITH C-33') (BY SIMILARITY).

INTERCHAIN (WITH C-32') (BY SIMILARITY).

INTERCHAIN (WITH BETA) (BY SIMILARITY).

INTERCHAIN (WITH ALLHA) (BY SIMILARITY).

INTERCHAIN (WITH BETA) (BY SIMILARITY).

INTERCHAIN (WITH ALLHA) (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                  Score 44.5; D
Pred. No. 31;
4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                     Length 438;
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                                                                                                                                                                                                                                                                                                     Indels
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: мау 9, 2000, 22:27:16; Search time 64.29 Seconds (without alignments)
26.447 Million cell updates/sec

US-09-104-340-3 147 1 MDCQLSILLLLSCS

Title: Perfect score: Sequence:

MDCQLSILLLSCSVLDSFGELIPQPSNE 29

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters:

168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database : PIR_63:*
1: pir1:
2: pir2:
3: pir3:
4: pir4: pir1: *
pir2: *
pir3: *
pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

30		20	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	σ	· UI	4	ω	2	۲		No.	Result
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site-specific	Ton-cransporting	1017010101	۲.	DNA (cytosine-5-	hypothetical	DNA polymerase	N-methylhydantoina	pulmonary surfac	surfactant p	FAD synthetase	hypothetical	hypothetical	₽.		permease 1 -	hypothetical	DNA nucleotidylexo	hypothetical	interferon alpha-	DNA (cytosine-5-	tryptophan synthas	hypothetical	hypothetical	₽.		AcOrf-91 pro	cartilage ma	Ρ-	receptor tyre	protein-tyrosine	•	Description	
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receptor tyrosine kinase Mek4 - mouse
C:Species: Mus musculus (house mouse)
C:Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C:Accession: A45583
R:Sajjadi, F.G.; Pasquale, E.B.; Subramani, S.
New Biol. 3, 769-778, 1991
A;Title: Identification of a new eph-related receptor tyrosine kinase gene from mouse A;Reference number: A45583; MUID:92031278
A;Recession: A45583
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-983 <SAJ>
A;Cross-references: GB:M68513; NID:g199119; PIDN:AAA39521.1; PID:g199120

45	44	43	42	41	40	39	38	37	36	ω	34	33	32	31
43	43	43	43	43.5	44	44	44	44	44	44	44.5	44.5	44.5	44.5
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Ig kappa chain pre	hypothetical prote	pRF2 protein - hum	seminalplasmin pre	hypothetical prote	DNA (cytosine-5-)-	hypothetical prote		hypothetical prote	probable olfactory	hypothetical prote	ATP-driven ion pum	probable amino aci	fibrinogen gamma c	H+/K+-exchanging A

ALIGNMENTS

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A; Gene: CMP
C; Superfamily: v
F; 1-29/Domain: s
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                                                                                                                                                                                                                                                                                                 Eur. J. Biochem. 236, 970-977, 1998
A;Title: Cloning, sequencing and expression analysis of mouse cartilage matrix protein
A;Reference number: 866522; MUID:96270751
                                                                                                                                                                                                                                                                                                                                                                                        cartilage matrix protein precursor - mouse c;Specles: Mus musculus (house mouse) C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 C;Accession: S66522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein C01G6.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 *sequence_revision 15-Oct-1999 *t.C;Accession: T18835
                                                                                        F;30-500/Product: cartilage matrix protein #status predicted < F;43-210/Domain: von Willebrand factor type A repeat homology F;231-266/Domain: EGF homology <EGF>
                                                                                                                                                                                                          A;Cross-references: EMBL:U35035; NID:g1163178; PIDN:AAB06521.1; PID:g1163179 C;Genetics:
                                                                                                                                                                                                                                           A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-500 <ASZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z35595; PIDN:CAA84634.1; GSPDB:GN00020; CESP:C01G6.3 A;Experimental source: clone C01G6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-495 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; translated
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                                                                                                                                            von Willebrand factor type A repeat homology; signal sequence #status predicted <SIG>
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                                                                           von Willebrand
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30-Apr-1999

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hypothetical protein F26B6.11 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change C;Accession: T01135
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T01135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
B45583
                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:M68514; NID:g454809; PIDN:AAA48666.1; PID:g211447 A;Note: sequence extracted from NCBI backbone (NCBIN:62405, NCBIP:62411) C;Superfamily: protein-tyrosinese, receptor type eph; fibronectin type C;Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein F;619-885/Domain: protein kinase homology <KIN>F;627-635/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Title: Identification of a new eph-related A; Reference number: A45583; MUID:92031278 A; Accession: B45583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor tyrosine kinase Cek4 - chicken C;Spectes: Gallus gallus (Chicken) C;Spectes: Gallus gallus (Chicken) C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999 C;Accession: B45583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Ayres, M.D.; Howard, S.C.; Kuzio, Virology 202, 586-605, 1994
A; Title: The complete DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Note: dsDNA virus
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 12-Nov-1999
C;Accession: D72861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Sajjadi, F.G.; Pasquale, New Biol. 3, 769-778, 1991
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A; Residues: 1-224 < AYR>
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A; Residues: 1-983 <SAJ>
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0; MUID:94303173
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C:Species: Caenorhab
C:Date: 15-Oct-1999
C:Accession: T28131
R:Berks, M.
                                                                                      A;Reference number: 219237
A;Accession: T20204
A;Status: preliminary; translated from
A;Molecule type: DNA
A;Residues: 1-399 <WIL>
                                                                                                                                                                                              hypothetical protein C54C8.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T20204 R;Dobson, R.
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A;Experimental source: cultivar Columbia
C;Genetics:
                                                                                                                                                         submitted to the EMBL Data Library, A; Reference number: 219237
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A; Introns: 358/3;
A; Note: F26B6.11
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A;Description: Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence.
A;Reference number: Z14198
A;Accession: T01135
                                      A; Experimental source: C; Genetics:
                                                                         A; Cross-references: EMBL: Z83102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: C; Genetics:
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A; Residues: 1-147 <WIL>
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A; Residues: 1-901 < ROU>
       A; Map
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nes 9; Conserv
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se: clone ZK970
                                                      clone
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                                                      102; PIDN:CAB05466.1; GSPDB:GN00019; CESP:C54C8.4 C54C8
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Pred. No. 24;
3; Mismatches
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Pred. No.
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R; Smith, D.R.; Douce
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Best Local
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A;Molecule type: mRNĀ
A;Residues: 1-1622 <KIM>
A;Cross-references: DDBJ:AB012214
C;Keywords: methyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                               DNA (cytosine-5-)-methyltransferase (EC 2.1.1.37) - C:Species: Rattus norvegicus (Norway rat) C:Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tryptophan synthase, beta subunit homolog - Methanobacterium thermoautotrophicum (str C;Species: Methanobacterium thermoautotrophicum C;Spate: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                          Biochem. Biophys. Res. Commun. A;Title: Expression of rat DNA A;Reference number: JE0378
A;Accession: JE0378
                                                                                                                                                                                                                                                                                                                                                       R;Kimura, H.; Takeda, T.; Tanaka, S.;
Biochem. Biophys. Res. Commun. 253, 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: tryptophan synthase beta chain; tryptophan synthase F;30-422/Domain: tryptophan synthase beta chain homology <TRPB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE000908; GB:AE000666; NID:g2622579; PIDN:AAB85951.1; PID:g262
A;Experimental source: strain Delta H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence
A;Molecule type: DNA
A;Residues: 1-429 <MTH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta A; Reference number: A69000; MUID:98037514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     137 QWGTALSLACSLMDLQCKVYMVRVSFNQKPFRKTIMQLYGGEVVPSPSN 185
                                       2 DCQLSILLLISCSVLDSFGELIPQ 25
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DCNVLLKLVMAGEVTNSLGQRLPQ
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Pred. No.
                                                                                                   Score 47; DB 2;
Pred. No. 1e+02;
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Pred.
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  1218
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495-501, 1998
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27;
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25;
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interferon alpha-1 precursor - pig
c;Species: Sus scrofa domestica (domestic pig)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C;Accession: S23709; 146589
R;Mege, D.; Lefevre, F.; Labonnardiere, C.
J. Interferon Res. 11, 341-350, 1991
A;Title: The porcine family of interferon-omega: cloning, structural analysis, A;Reference number: S23709; MUID:92193689
A;Accession: S23709;
                                                                                       RESULT
B23595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
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J. Interferon Res. 6, 349-360, 1986
A;Title: Molecular cloning and sequencing of a gene encoding A;Reference number: 146589; MUID:87035119
A;Accession: I46589
    DNA nucleotidylexotransferase (EC 2.7.7.31) - mouse
N;Alternate names: terminal addition enzyme; terminal deoxyribonucleotidyltransferase
C;Species: Mus musculius (house mouse)
C;Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 18-Jun-1999
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A; Accession: T38260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein SPAC23C4.05c - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T38260
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A; Residues: 1-189 < LEF>
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A; Residues: 1-189 <MEG>
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les 8; Conserv
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10; Conserv
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72.78;
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Pred. No.
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September 1997
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02-Jun-1988 #text_change 18-Jun-1999
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16;
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37;
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A;Residues: 1-25,'M',27-98,'F',100-192,'R',194-286,'Q',288-308,'E',310-366,'D',368-44
A;Cross-references: EMBL:X68670; NID:g287808; PIDN:CAA48634.1; PID:g287809
C;Superfamily: DNA nucleotidylexotransferase
C;Keywords: alternative splicing; magnesium; nucleotidyltransferase; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:X04123; NID:g54765; PIDN:CAA27735.1; R;Doyen, N.; d'Andon, M.F.; Bentolila, L.A.; Nguyen, Q.T.; F. Nucleic Acids Res. 21, 1187-1191, 1993
A;Title: Differential splicing in mouse thymus generates two A;Reference number: S30235; MUID:93219079
A;Accession: S30235
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R;Koiwal, O.; Yokota, T.; Kageyama, T.; Hirose, T.
Nucleic Acids Res. 14, 5777-5792, 1986
A;Title: Isolation and characterization of bovine
A;Reference number: A93633; MUID:86286588
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A; Introns: 51/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein Y53C12B.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T27133
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A; Residues: 1-529 < KOI>
                                                                                                                                                                                                                                                           A;Cross-references: EMBL:299278; PIDN:CAB16490.1; GSPDB:GN00020; CESP:Y53C12B.1
A;Experimental source: clone Y53C12B
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A; Residues: 1-793 <WIL>
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Matches 10
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                                     1 MDCQL-----SIL------LLLSCSVLDS--FGELIPQPSNE 29
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LDCQLIRGHTESVLSVVSPTWDTSLLASCSKDNSIIFWRLVTSPEND
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                                                                             l Similarity
16; Conserv
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10; Conser
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                                                                               Conservative
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                                                                           Score 46; DB Pred. No. 69; 5; Mismatches
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Pred. No.
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/

2: /cgn2_6/ptodata/
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Match
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/cgn2_6/ptodata/2/iaa/6_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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      BB
 US-08-167-919A-10
US-08-749-645A-21
US-08-715-106-10
US-08-715-106-11
US-08-715-106-12
US-08-6167-919A-2
US-08-6167-919A-3
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Sequence 10, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 3, Appl
Sequence 3, Appl
Sequence 4, Appl
Sequence 4, Appl
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Sequence 4, Appl
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Sequence 6, Appl
Sequence 6, Appl
Sequence 125, App
Sequence 125, Appl
Sequence 127, Appl
Sequence 127, Appl
Sequence 128, Appl
Sequence 129, Appl
Sequence 130, Appl
Sequence 131, Appl
Sequence 131, Appl
Sequence 131, Appl
Sequence 131, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 31, Appl
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Result No.

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27.6	27.6	27.6	27.9	27.9	27.9	27.9	27.9	27.9	27.9	27.9	27.9	28.6	28.6	28.6	28.6
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US-08-468-413-2	US-08-729-103-1	US-08-194-981E-14	US-08-680-326-33	PCT-US94-14989-2	US-08-452-734A-2	US-08-453-862-2	US-08-702-367A-29	US-08-449-645A-29	US-08-396-957A-4	PCT-US93-08528-68	US-08-118-270-68	US-08-444-644-25	US-08-444-644-15	US-08-487-200-31	US-08-474-040-31
Sequence 2, Appli	Sequence 1, Appli	Sequence 14, Appl	Sequence 33, Appl		Sequence 2, Appli	2	Sequence 29, Appl	•	Þ	Sequence 68, Appl				31,	

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TOPOLOGY: linear MOLECULE TYPE: protein	LENGTH: 983 amino acids	CTERISTICS:	INFORMATION FOR SEC ID NO: 10:	; ;	თ	H	CKET NUMBE	Ä		AGENT	FILING DATE: 19-JUN-1992	2	FILING DATE: 12-DEC-1991	N	A:	N-1991	APPLICATION NUMBER: PK6841 (AU)	_	•	×	APPLICATION NUMBER: US/08/167.919A	CURRENT APPLICATION DATA:	BatoatTa Bologga #1 0 Worston #1	IBM PC c	TYPE: Flo	Ħ	5	ĸ	. New Y	Garden City	STREET: 400 Garden City Dlaza	Ontt Kirrhing	NORDERODONTENOS ADDRESOS 14	NVENTION: A	OF INVENTION: A NO	CANT: Wilkinson, David	••	Wicks, I	Simpson, Ric	APPLICANT: Boyd, Andrew W.	GENERAL INFORMATION:	sequence 10, Application Us/U816/919A Patent No. 5674691	US-U8-167-919A-10	

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US-08-702-367A-21
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                                                                                                                             Patent No. 5981246
GENERAL INFORMATION:
APPLICANT: FOX, G
                                                                                                                                                             Sequence 21, Application US/08702367A Patent No. 5981246
                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                            Query Match
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GENERAL INFORMATION:
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: A INFORMATION FOR SEQ ID NO: 21: SEQUENCE CHARACTERISTICS: LENGTH: 983 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC -DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
FILING DATE:
CLASSIFICATION: 435
                                                                                                  APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy
                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Fox, Gary M.
STREET: 10*V CITY: Thousand Oaks
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine ITLE OF INVENTION: Kinases
                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
TOPOLOGY: 11r
                                                                                                                                                                                                                                                                                                            Match 100.0%;
Local Similarity 100.0%;
les 29; Conservative 0;
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29; Conserv
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                                        E: Amgen Patent Operations/RBW 1840 Dehavilland Drive
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1840 Dehavilland Drive
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Pred. No. 2.2
0; Mismatches
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Pred. No. 2.2e-14;
D; Mismatches 0;
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.2e-14;
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FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERRINCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
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                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 100.0%;
les 29; Conserva+""
                                                                                                                                                                                                                                                                                                            COUNTRY: U
ZIP: 11530
                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                       CITY: Garden City
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                               APPLICATION NUMBER:
                        APPLICATION NUMBER:
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SOFTMARE: PATENTIAL Release #1.0, Version #1.25
SOFTMARE: DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/715,106
FILING DATE: 18-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,919
FILING DATE: 18-ARR-1994
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Simpson, Richard J.
APPLICANT: Wicks, Ian
APPLICANT: Ward, Larry D.
APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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MBER: PCT/AU92/00294
19-JUN-1992
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                                                                      PK9992 (AU)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 147; DB 2;
Pred. No. 2.2e-14;
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TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-04681-21
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PCT-US95-04681-21
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                                                                 Matches
                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 21, Application PC/TUS9504681 GENERAL INFORMATION:
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Best Local 9
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                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 21
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 10:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1840 CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acids
TYPE: amino acid
TOPOLOGY: line-
fOLECTIVE
                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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LENGTH: 983 amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                             Local Similarity
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CLASSIFICATION:
                                                                                                                                                                                                          TYPE: amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: DiGiglio, Frank REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MDCQLSILLLLSCSVLDSFGELIPQPSNE 29
                  MDCQLSILLLLSCSVLDSFGELIPQPSNE 29
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MDCQLSILLLSCSVLDSFGELIPQPSNE 29
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1840 Dehavilland Drive
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(516) 742-4366
                                                                Conservative
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                                                                           100.0%;
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                                                            Score 147; DB 4;
Pred. No. 2.2e-14;
); Mismatches 0;
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                                                                                           Length 983;
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                                                            Indels
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US-08-162-809-16
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                                                                                                                                                                                                      Sequence 16
Patent No.
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Best Local
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                                                                              GENERAL INFORMATION:
APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS O
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ZHOU,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 08/1 FILING DATE: 04-JAN-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: METHODS NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ZHOU, RENPING; SCHULZ, NICHOLAS, APPLICANT: T.; KROMER, LAWRENCE, F.; VANDE WOUDE, APPLICANT: GEORGE, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: AMINO ACID
STRANDEDNESS: UNI
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                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
 COUNTRY:
                                 CITY: San Diego
                                                 STREET:
                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                        9 LLLSCSVLDSFGELIPQPSNE 29
||| |: | | | | :| ||
8 LLLLCAALGSAGRLSARPGNE 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                       16, Application US/08162809
5. 5457048
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                                            E: CAMPBELL AND FLORES, 4370 La Jolla Village Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
United States of America
                                                                                                                                                                                                                                                                                                                                                                               Conservative
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52.4%;
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TYROSINE KINASE AND LIGAND AND THEIR
USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
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                                                                                                                  METHODS OF USE
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-162-809-16
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US-08-167-919A-2
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                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNUBER: PK6841 (AU)
FILLING DATE: 21-JUN-1991
PRIOR APPLICATION UNUBER: PK9992 (AU)
FILLING DATE: 12-DEC-1001
PRIOR APPLICATION UNUBER: PK9992 (AU)
PRIOR APPLICATION UNUBER: PK9992 (AU)
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Best Local Similarity
Watches 11; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: BOYD, ANDI
APPLICANT: Simpson, F
APPLICANT: Wicks, Iar
APPLICANT: Ward, Larr
APPLICANT: Wilkinson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08167919A Patent No. 5674691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (619) 535-89. INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/08/167,919A
FILING DATE: 18-APR-1994
                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: P-LJ 9503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
TELEPAX: (619) 535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                             ZIP: 11530
                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                APPLICATION NUMBER:
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MBER: PCT/AU92/00294
19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Andrew W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Richard J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (516) 742-43
TELEX: 230 901 SANS U
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08
APPLICATION NUMBER: 18 APPLICATION NUMBER: PFILING DATE: 21-JUN-18
                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                             APPLICATION NUMBER: PK9992 (AU) FILING DATE: 12-DEC-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
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LENGTH: 14 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: (516) 742-4343
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                                                                         FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                               PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE TITLE OF INVENTION: AND USE THEREOF
             NAME: DIGIGIIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCY,DOCKET NUMBER: 9159
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/01
FILING DATE: 18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Garden City
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                                                                                                              APPLICATION NUMBER: PCT/AU92/00294
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Ward, Larry D.
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(516)
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1 SANS UR
NO: 2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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US-08-167-919A-3
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Best Local Similarity 100.
""" onservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                  TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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LCTERISTICS:

LYPE: amino acid

STANDEDNESS: si

TOPOLOGY:

OLECULF

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                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,919A
FILING DATE: 18-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Boyd, Andrew W.
APPLICANT: Simpson, Richard J.
APPLICANT: Wicks, Ian
APPLICANT: Wards, Larry D.
APPLICANT: Wikinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
                                                                                                                                REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9159
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                      APPLICATION NUMBER: PK9992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-UN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DiG1g110, Frank S.
                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PK68.
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
                                 SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS: ADDRESSEE: Scully, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 ELIPQPSNE 29
                                                                                                                                                                      REGISTRATION NUMBER:
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5, 5674691
              amino acid
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                              19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (516) 742-4366
                                                                                                                    (516) 742-4343
single
                                                                                                                                                                                    Frank
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100.0%; Pr
                                                                                                                                                                                                                                                                                                                                            PK6841 (AU)
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0.26;
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Query Match
Best Local Similarity
Watches 9; Conserve
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US-08-715-106-3
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                                                                                                                                                                                                                 PILING DATE: 21-JUN-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK9992 (AU)
EILING DATE: 12-DEC-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU92/00294

FILING DATE: 19-CUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/715,106
FILING DATE: 18-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,919
FILING DATE: 18-APR-1994
APPLICATION NUMBER: PK6841 (AU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                               TELEX: 230 901 SANS UR INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wicks, Ian
APPLICANT: Ward, Larry D.
APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
                                            SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                             TELECOMMUNICATION INFORMATION: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                               TELEFAX:
                              TOPOLOGY:
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                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Scully, Scott, Murphy & Presser
400 Garden City Plaza
                                                                                                                                                 2: (516) 742-4343
(516) 742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Simpson,
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                               linear
            protein
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. 0.37;
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Query Match Best Local Similarity

32.0%; 100.0%;

Score 47; Pred. No.

DB 3; 0.37;

Length 19;

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RESULT 13
PCT-US95-07372-12
; Sequence 12, Application PC/TUS9507372
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                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/476,275
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,099
FILING DATE: 03-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 01:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 03-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,891
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 22314
COMPUTER READABLE FORM:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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: Newman, Roland A.
: Reff, Mitchell E.
: Rastetter, William H.
: Rastetter, William H.
INVENTION: Therapeutic Application of INVENTION: Radiolabeled Antibodies to INVENTION: Differentiation Antigen for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               699 Prince St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 amino acids
                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BURNS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
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                                                                                                                                                                                                                                                                                        Score 45; DB Pred. No. 6.7; Mismatches
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to Human B Lymphocyte Restricted
for the Treatment of B-Cell
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; OTHER INFORMATION: /note= "Gln at position 23 starts; OTHER INFORMATION: mature peptide." PCT-US95-07372-12
                                                                                                                                                                                                                                                      RESULT 14
US-08-827-291A-2
                                                                                                                                                                                                             Sequence 2, Application US/08827291A Patent No. 5874243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMER
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404) 873-8794
TELEPHONE: (404) 873-8795
INFORMATION FOR SEQ ID NO: 12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Macina, Roberto
APPLICANT: Sathe, Ganesh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Oklaho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTY 30309-3430
ZIP: 30309-3430
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACTIBLE
COMPUTER: TYPEM: PC-105/MS-DOS
            NUMBER OF SEQUENCES: NOVEL OLRCC15 RECEPTOR SEQUENCES: 2
CORRESPONDENCE ADDRESS: ADDRESS: Smithkline Beecham Corporation STREET: 709 Swedeland Road CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL: NO ANTI-SENSE: NO FRAGMENT TYPE: N-terminal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 129 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Oklahoma Medical Research Foundation TITLE OF INVENTION: Calcium Binding Recombinant TITLE OF INVENTION: Antibody Against Protein C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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STREET: 2800 One Atlantic Center
STREET: 1201 West Peachtree Street
CITY: Atlanta
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
COUNTRY:
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|| |: | ||:| ||: | |::|
1 MDFQVQIFSFLLISASVIMSRGQII 25
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Pred. No.
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COMPUTER READABLE FORM: MEDIUM TYPE: Diskett

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US-08-207-904-2
; Sequence 2, Application US/08207904
; Patent No. 5477002
                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/207,904
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION NUMBER: US/07/908,242
APPLICATION NUMBER: US/07/908,242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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APPLICANT: Tuttle, AnnMarie
APPLICANT: Crossland, Lyle D.
TITLE OF INVENTION: Anther-Specific cDNA Sequences, Genomic
TITLE OF INVENTION: DNA Sequences and Recombinant DNA Sequences
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 316 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,291A
FILING DATE: 28-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lazar, Steven R.
REGISTRATION NUMBER: 32,618
REFERENCE/DOCKET NUMBER: CGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: GP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5015
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PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 CELPSILILSCNDTSIFEKVI 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 42.9%; les 9; Conservation
                                                                                                                                                                                                                                                                                                                 CITY: Hawthorne
STATE: New York
                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: sir
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REGISTRATION NUMBER: 30,954
                                                                                                                                                                                                                                                                                  ZIP: 10532
                                                                                                                                                                                                                                                                                                    COUNTRY:
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Search completed: May
Job time: 4149 sec
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                                                                                                                                                                                    ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-207-904-2
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TELEPHONE: (919)541-8615
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 448 amino acids
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Best Local S
                                                                                                                      Matches
                                                              Local Similarity nes 9; Conserv
                                                                                        1 MDCQLSILLLLSCSV---LDSFGELIPQP 26
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Post-processing: Minimum Match 0%
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9, 2000, 21:52:03; Search time 50.71 Seconds (without alignments)
13.546 Million cell updates/sec
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W88379
R75711
R753731
W58379
W483902
W73231
R75214
W73261
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R75214
R75260
R755214
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Human cytochrome p
Human derived cyto
Human metabotropic
Murine variable re
Human olfactory OL
Polypeptide encode
Tobacco Ant32 geno
Mouse 5C7.29 monoc
Variable region of
Sequence encoded b
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Mouse L6 antibody
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Eph-related PTK Ce
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Human sperm-specif
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Result No.

Score

Database :

Minimum DB Maximum DB

Searched:

Scoring table:

Sequence: Title: Perfect score: Run on:

4 <u>4</u> 51	44	43	42	41	40	39	38	37	36	35
43	43	43	43	43	43	43	43	43	43	43
29.3	29.3	29.3	29.3	29.3	29.3	29.3	29.3	29.3	29.3	29.3
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W31949	W31950	W23596	W83431	W83428	W73315	R92276	R27705	R76699	R76700	W73314
Human bg protein a	Human bo protein a	Human LYST1 longer	Rat Munc13-1. Scre	Munc13-1-interacti	Parathyroid hormon	Opossum kidney PTH	Opossum kidnev PTH	ShET2 enterotoxin	EIET enterotoxin e	Parathyroid hormon

ALIGNMENTS

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Claim 6; Fig 1; 58pp; En Claim 6; Fig 1; 58pp; En This sequence represets expressed in both pre-B tumours of human origin, and the epithelial tumou (TK) and/or its ligands	Receptor-type tyrosine kinase re- III-A4 - is EPH-ELK-like Kinase, proteins in modulating pre-B, B in therapy etc.	WPI; 93-036373/04. P-PSDB; R31466.	(HALL-) HALL INST	9-JUN-1992; 1-JUN-1991;	WO9300425-A.	modified_site 7	binding_site 6	binding_site 6	binding_site 6	domain 5	modified_site 4	modified_site · 4	modified_site 3	modified_site 3	modified_site 2	protein 8	protein 2	tide	Homo sapiens.	TK; ligand; B;cel	<pre>Lila-1: TM: enith</pre>	Primer; expressio	24-MAY-1993 (fir	R31466 standard; R31466;	JLT 1 166
1; 58pp; English. represets human eph/elk-like kinase (HEK). HEK is both pre-B cells and T cell lines and in a number of man origin, eg. lymphoid tumours LK63, Lila-1 and JM, elial tumour HeLa. This receptor-type thymidine kinase ts ligands are useful as agents in modulation of the	osine kinase reactive with monoclonal antibody LK-like kinase, useful for phosphorylating ating pre-B, B and T cell function, in cancer	Wicks I	MEDICAL RES WALTER & ELI	AU0294. AU-006641.	note= "Putative autophosphorylation site"	"ATP binding site"	"ATP	"ATP binding site	"Tran	"N-link glycosylation	"N-link glycosylation	-link	"N-link glycosylation	<pre>/note= "N-link glycosylation" 337339</pre>	"Purified HEK protein	50 Furtited HEN Protein #1	"Signal peptide"	, Marti	Oration /Oualifions	B; cellular response; growth; differentiation.	l; T; tumour; lymphoid; LK63;	vector; ex	st entry)	Protein; 983 AA.	

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RESULT
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ID 381
AC WI
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FPN W
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Matches 14
30-DEC-1998:
17-JUN-1998: E04016.
19-JUN-1997: EP-201863.
(ALKU ) AKZO NOBEL NV.
AICKEN RJ, GEOCHENHUIS AJ, V
WPI: 99-095361/08.
N-PSDB; x06779.
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17-JUN-1998; E04016.
19-JUN-1997; EP-201863.
(ALKU ) AKZO NOBEL NV.
Aitken RJ, Grootenhuis AJ, Van D
WPI; 99-095561/08.
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This is a partial sequence of human sperm specific antigen 4.1.

The sequence was deduced from a cDNA clone (see X06777) isolated from a human testicular cDNA library using marmoset 4.1 cDNA as probe. A full-length sequence for protein 4.1 is provided in W88380. Human and marmoset sperm protein 4.1 and 6.7 (see W88373-80) and nucleotide sequences (see X06772-79) encoding them are new. The proteins are sperm specific and can be used in a contraceptive vaccine to prevent or reduce fertility in a subject without the autoimmune reactions that are a serious side-effect of the sequence of the sequ
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W88378
                                                                                                                                                                                                                                                                                              Human sperm-specific antigen 4.1. Sperm-specific antigen 4.1; vacci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        production and/or function analogues have activity in cellular responses such as Sequence 983 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     W88380 standard; Protein;
W88380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prior art female contraceptive host cells used in production c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; X06777
                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                               26-APR-1999 (first entry)
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58.38;
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vaccine; contraceptive; human.
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smatches 0;
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0.88;
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R75711;
11-NOV-1995 (first er
Eph-related PTK Cek4.
Cek4; Eph; protein ty;
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This is a full-length sequence of human sperm specific antigen 4.1 The sequence was deduced from a cDNA clone (see X06777) isolated from a human testicular cDNA library using marmoset 4.1 cDNA as probe. Human and marmoset sperm proteins 4.1 and 6.7 (see W88373-80) and nucleotide sequences (see X06772-79) encoding them are new. The proteins are sperm specific and can be used in a contraceptive vaccine to prevent or reduce fertility in a subject without the autolamune reactions that are a serious side-effect of prior art female contraceptive vaccines. Expression vectors and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 85-89; 129pp; English.

Probes derived from the EPH-related PTKS Cek4 (Q90659) and Ce (Q90660) were used to isolate novel CDNA clones (Q90652-58, Q90661-62) from chicken embryo and embryonic brain libraries. Cek4 is highly expressed in the chicken developing brain and embryonic tissues and also in the adult brain and retina. Sequence 983 AA;
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07-SEP-1994; U10140.

03-DEC-1993; US-162809.

(LJOL-) LA JOLLA CANCER RES FOUND.

Pasquale EB, Sajjadi FG;

WPI; 95-215256/28.
                                                                             Key
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R75711;
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W09515375-A.
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                                                                                                                                                                                                                                                                                                                                    9 LLLSCSVLDSFGELIPQPSNE
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8 LLLLCAALGSAGRLSARPGNE
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p170-2;
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                                                                        sequence of p170-2 comprising soluble T4 protein; AIDS; ARC; Location/Qualifiers
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                        /label=T4 surface glycoprotein
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                                                                                                                                                                                                                08-JUN-1989; U02453.
10-JUN-1988; US-204645.
20-APR-1989; US-341080.
(GEHO-) General Hospital Corp
Fisher RA, Schooley RT, Hirsch M
WPI; 90-007302/01.
                                                                                                                                                                                                                                                                                                                                                                                        R04031;
29-MAY-1990 (first entry)
Full length T4 encoded by plasmid p170-2.
Soluble T4; p170-2; anti-retroviral agent
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 121pp; English.

Entire sequence from T4-encoding plasmid p170-2. It is almost identical to the sequence published by Maddon et al. (1985) with the exception of three codon changes. At T4 amino acid residue 3, (posn.403 of entire sequence) Lys is encoded in stead of Asn. At posn. 64, (posn.464) Arg replaces Trp and at posn. 231, (posn. 631) Ser replaces Phe.
                                                                              ARC and HIV infection.

Disclosure; fig 1; 100pp; English.

Disclosure differs from that determined by PJ Madden et al., [Cell, 42 pp. 93-104 (1985)] in three places due to three nucleotide substitutions. The Asp reported at position 3 by Madden et al. was the result of a sequencing error [DR Littman et al. Cell, 55, p.541 (1988)].

X = stop codon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2268
       The sequence was deduced from the cDNA insert of p170-2. Soluble T4 constructs may be produced by truncating this sequence is fragments from position 400 to 799, removing the transmembrane and intracytoplasmic domains whilst retaining the extracellular region responsible for HIV binding. The sol. T4 is combined with an anti-
                                                                                                                                                                    Combinations of soluble T4 protein and anti-retroviral agent having symergistic activity in treatment and prevention of A
                                                                                                                                                                                                      N-PSDB; Q03005
                                                                                                                                                                                                                                                                                                 WO8911860-A.
14-DEC-1989.
                                                                                                                                                                                                                                                                                                                                          misc_difference
                                                                                                                                                                                                                                                                                                                                                                   misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soluble T4 can be produced by truncating the CDS to remove the transmembrane and cytoplasmic domains. The soluble forms may be modified to increase their immunogenicity by addition of an adjuvant such as incomplete Freund's adjuvant. The T4 interferes with HIV/T4 interaction and elicits anti-soluble T4 antibody production.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treating or preventing AIDS, ARC or HIV infection administering an immunologically effective amt. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUL-1990.
18-JAN-1990; U00358.
18-JAN-1989; US-300096.
(HARD) HARVARD COLLEGE.
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13; Conser
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: 423
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653
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Pred. No. 95;
4; Mismatches
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(S, Johnson VA,
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Walker
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4 149

QHCIILLSCHPQDAFLXLVSTQPSH

174

QLSILLLSCSVLDSFGELI-PQPSN

28

Matches

Match

Similarity

32.3%;

Score Pred.

47.5; No. 9

Length 242;

6; BB

Conservative

4:

Mismatches

8

Indels

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Gaps

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RESULT
W58379
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PT New compositions for immuno-therapy and protection - comprise PT nucleotide sequences encoding an immuno-modulating protein and an PT antigen, used for e.g. infections, cancer or auto-immune diseases PS Example 6; Fig 14; 136pp; English.

CT he present sequence represents the protein from the third reading CT frame of human immunomodulatory protein BL-1 encoding cDNA (given in CC v30915). The present invention describes a plasmid which comprises a cnucleotide sequence (NS) that encodes:(a) an immunomodulating protein Selected from interleukin (II)-12, granulocyte-macrophage colony CC stimulating factor (GM-CSF), IL-1), IL-15, IL-18, and BL-1 operably CC INF- beta, IL-2, IL-4, IL-5, IL-10, IL-15, IL-18 and BL-1 operably CC inked to induce an immune response to an antigen such as a pathogen can be used to induce an immune response to an antigen such as a pathogen colony can be used for immunotherapy or to provide a protective immune color response. In particular, they can be used for treating subjects with careful as cancer or psorlasis or autoimmune diseases or an allergen careful reaction, pathogen infection, hyperproliferative disease cancer or psorlasis or autoimmune diseases e.g. rheumatoid component diabetes mellitus, autoimmune thyroiditis, ankylosing color casculitis, Wegener's granulomatosis, Crohn's disease and ulcerative coloris, Grave's disease, autoimmune thyroiditis, askthma and colorisis of colorisis anadmane allocases and ulcerative colorisis of colorisis of sequence 242 AA;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        (APOL-) APOLLON INC.
(UYPE-) UNIV PENNSYLVANIA.
Bagarazzi ML, Boyer JD, Ki
WPI; 98-261495/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immunomodulatory protein BL-1 Human; BL-1; immunotherapy; vaccine; infection; cancer; autoimmune disease
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23-OCT-1997; U19502.
23-OCT-1996; US-028613.
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    frame of BL-1 cDNA and
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No. 95;

    immunomodulatory protein; HIV;

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WRESULT IN A SALE PROPERTY OF THE PROPERTY OF 
       RESULT W732311 ID W73231 W7 AC W7 AC
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Best Local
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03-NOV-1998
19-MAY-1995; 444454.
02-OCT-1987; US-104461.
02-OCT-1982; US-355298.
01-NOV-1982; US-43128.
23-AUG-1991; US-43127.
11-SEP-1992; US-949327.
11-MAY-1995; US-444454.
   US5827694-A.
27-OCT-1998.
19-MAY-1995;
02-OCT-1987;
08-MAR-1982;
01-NOV-1982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 14A; 48pp; English.

This is the amino acid sequence of porcine interferon alpha-1, as deduced from the open reading frame of a cDNA clone (see V68167). The invention provides bovine, murine, porcine, feline, laprine and rat mature alpha, beta and gamma interferons and their propeptides (see W83895-905, W83918 and W70582-85). Recombinant DNA methods can be utilised to prepare these non-human animal interferons in amounts sufficient to enable the determination of their blochemical properties and bloactivities, and hence to allow efficient production for commercial or biological exploitation. Interferons are useful as antiviral and antitumour agents.
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Capon DJ, Goeddel DV;
WPI; 99-007993/01.
N-PSDB; V68167.
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W83902;
15-FEB-1999 (fir
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01-MAR-1999
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Interferon-alpha 1; leukocyte interferon; virucide; antiviral;
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446171.
US-104461.
US-395298.
US-438128.
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/label= Sig_peptide
24. .189
/label= Mat_protein
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/label= Mat_prote
/note= "Claim 1"
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Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   interferon; virucide; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₿
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expressing human cytochrome p450 and a yeast NADPH-P450 reductase

PS Examples; Page 23-25; 124pp; English.

CC cDNA was amplified by PCR using the primers 087735-8. The product was

CC cloned into the yeast expression vectors pAAH5N or pAHRR to produce the

CC vectors p2C9 for the expression of the cytochrome P450 alone or p2C9R

CC for co-expression with the yeast NADPH-P450 reductase.

CC The vectors are used in a method for evaluating the safety of a chemical

CC compound by reacting the chemical compound with recombinantly produced

CC human cytochrome P450 molecular species and variants (087716)

CC or 3A4 (087717), or their auxillary species and variants (087718-32), and

CC yeast NADPH-P450 reductase, either as a fused protein or in cell

CC extracts, and analysing the resulting metabolite to assess the safety of

CC the chemical compound. The method is useful for determining whether and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 6; Fig 14A; 59pp; English.

CC This is the amino acid sequence of porcine interferon alpha-1,

CC deduced from a cDNA (see V08184). The invention provides

CC bovine, porcine, feline and rabbit mature interferons and their

CC propeptides (see W73224-35). Recombinant DNA methods can be used

CC propare these non-human animal interferons in amounts sufficient

CC to enable the determination of their biochemical properties and

CC bioactivities, and hence to allow efficient production for

CC commercial or biological exploitation. Interferons are useful as

CC antiviral and antitumour agents. A replicable expression vehicle

CC comprising claimed non-human animal interferon nucleic acid, a

CC process for producing such an interferon, and a microorganism

CC (especially Escherichia coli) or cell culture transfected with the

CC nucleic acid are claimed.
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21-SEP-1992; US-949327.

19-MAY-1995; US-446171.

(GETH ) GENENTECH INC.

Capon DJ, Goeddel DV;

WPI; 98-593994/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding non-human interferon polypeptide(s) - producing recombinant polypeptide(s) to determine t bioactivity
                                                                                                                                                                                                                                                           WPI; 95-116991/16.
N-PSDB; Q87715.
Evaluation of safety
                                                                                                                                                                                                                                                                                                                                                                               20-JUL-1994; 111298.
20-JUL-1993; JP-201120.
21-JUL-1993; JP-180246.
30-JUL-1993; JP-208279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cytochrome P450 molecular species 2C9 protein. Human cytochrome P450; amplification; PCR; primer; e yeast NADPH-P450 reductase; safety; fusion protein; carcinogen; mutagen; liver metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; V08184.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
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                                                                                                                                                                                                                                                                                                               Yabusaki
                                                                                                                                                                                                                                                                                                                                 Hayashi K,
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SUMITOMO CHEM
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fusion protein; metabolite;
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RESULT
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13-JUL-1994; 161551.
13-JUL-1994; JP-161551.
(SUMO) SUMITOMO CHEM CO LTD.
WPI; 96-136337/14.
N-PSDB; T17404.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Pages 11-13; 13pp; Japanese.

The present sequence is the human derived cytochrome (HDC) p4502c9, which was obtd. from a commercial cDNA library. Yeast were transfected with an expression vector contg. the HDC cDNA, cultured and then disrupted to give a microsomal fraction. The HDC was purified from the fraction, and used to immunise and sensitise a mammal. Blood was drawn from the mammal, and an anti-HDC antibody isolated. The antibody obtd. recognises HDC p4502c9, partic. at a serum dilution rate of 1:10000, and is substantially without cross reaction to other HDC p450 spp. . Sequence 490 AA;
                        05-MAR-1996.
15-JUL-1994;
20-JUL-1993;
30-JUL-1993;
                                                                                                                                                                                        11-007-1996 (LITEL ELLY)
Human cytochrome P450 molecular species 2C9 protein.
Human cytochrome P450; amplified; PCR; polymerase chain reaction; primer;
Human cytochrome P450; amplified; PCR; polymerase chain reaction; primer;
liver; yeast; expression vector; NADPH-P450 reductase; ADH gene promoter;
liver; yeast; expression vector; metabolite; detoxification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human derived cytochrome P4502C9.

Human derived cytochrome; P4502C9; commercial cDNA library; yeast; transfection; recombinant production; expression vector; mammal; immunisation; sensitisation; antibody; determination; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chemical compound, or its carcinogenic or mutagenic Sequence 490 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibody recognising human derived cytochrome P4502C9 - specific detection of cytochrome P450 species in humans Example 1; Pages 11-13; 13pp; Japanese.
                                                                                                                             J08056695-A.
                                                                                                                                                                                carcinogenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
J08027196-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R81465 standard;
                                                                                                                                                                                                                                                                                                           11-OCT-1996 (first entry)
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                                                                                                                                                                                                                                                                                                                                                              standard;
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13; Conser
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JP-201120.
JP-208279.
JP-136053.
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                                                                             164184.
                                                                                                                                                                                                                                                                                                                                                            Protein;
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Pred. No. 43;
6; Mismatches
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Pred. No. 43;
6; Mismatches
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RESULT
W27850
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Best Local
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This is the amino acid sequence of the human cytochrome P450 molecular Species 209 protein. The corresp. gene was amplified from a human liver derived cDNA library as 2 fragments of 0.9 and 0.6 kb using primers 725925-8. The prod. was cloned into the yeast expression vector PAAH5N to generate plasmid p209 for prodn. of the cytochrome only or into the vector pAHRR to generate the plasmid p209R for co-prodn. with the yeast vanney-p450 reductase. The sequence is placed under control of the yeast
Claim 6; pages 309-310; 989pp; English.

Claim 6; pages 309-310; 989pp; English.

The present sequence represents a Staphylococcus aureus protein of unknown function. The DNA sequence was isolated from a library of clones of S. aureus WCUH 29 in Escherichia coli. The DNA sequence can be used in the construction of ribozymes and antisense sequences to control the expression of Staphylococcal genes. The DNA sequence is also useful as a source of regulatory elements for the control of bacterial gene expression. The present protein may be used to produce vaccines to enable a host to produce specific antibodies with antibacterial action. These vaccines and antibodies would protect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADH gene promoter and terminator.

ADH gene promoter and terminator.

The vectors are used in a method for evaluating the safety of a cpd. by reacting the test cpd. with recombinantly produced human cytochrome P450 mol. species 1A2 (T28380), 2C9, 2E1 (T28382), 3A4 (T28383) or their mol. species 1A2 (T28380), 2C9, 2E1 (T28382), 3A4 (T28384-98) together with yeast NADPH-P450 reductase (either as variants (T28384-98) together with yeast NADPH-P450 reductase (either as
                                                                                                                                                                                                    aureus infection
                                                                                                                                                                                                                    Novel polypeptide(s) from to isolate antimicrobial c
                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                            Black MT, Burnham MK, Hodgson JE, Pratt JM, Reichard RW, Rosenberg 1 WPI; 97-424969/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus protein of unknown function.
Staphylococcus aureus protein; ribozyme; antisense sequence; control;
Staphylococcal gene; regulatory element; bacterial gene expression;
vaccine; Staphylococcal infection; food poisoning; scaled skin syndron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W27850 standard; Protein; 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rendered carcinogenic or "unsafe" if it is not detoxified metabolised to a carcinogenic cpd.
Sequence 490 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a fused protein or as a cell extract) and analysing the resultant metabolite. The cpd. is considered "safe" if it is detoxified or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel method for the evaluation of the safety of a cpd. - using a human cytochrome P450 and yeast NADPH reductase to determine whether the analyte cpd. is detoxified or metabolised to a carcinogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SUMO ) SUMITOMO C
WPI; 96-182311/19.
N-PSDB; T28381.
                                                                                                                                                                                                                                                                                                                                                       21-AUG-1997.
19-FEB-1997; U02318.
20-FEB-1996; US-011888.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc_difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         toxic shock syndrome.
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13; Conserv
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112
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                                                                                                                                                                                                                      compounds, and
                                                                                                                                                                                                                                        Staphylococcus aureus strain WCUH29
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Pred. No. 4
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Mismatches
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Matches 11
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Best Local Similarity 57.
Matches 8; Conservative
                      07-JAN-1998.
02-JUL-1997; 304821.
03-JUL-1996; US-021243.
(ELIL) LILLY & CO ELI.
Belagaje RM, Wu S;
WPI; 98-054913/06.
N-PSDB; V04206-07.
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Staphylococcal i
skin syndrome, a
Sequence 114 i
                                                                                                                                                                                                                                                                                                                                                                      causing rapid depletion of peripheral B cells, also new antibodies and hybridomas Disclosure; Fig 4; 101pp; English.

The sequence is the murine variable region light chain derived from murine anti-CD20 monoclonal antibody 2BS.

See also Q65529-35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reffme;
WPI; 94
                                                                                                                          Metabotropic glutamate receptor; mGluR8; human; agonist; antagonist; neurodegenerative disease; antipsychotic; anticonvulsant; analgesic; anxiolytic; antidepressant; antiemetic; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-NOV-1993; U10953.
13-NOV-1992; US-978891.
03-NOV-1993; US-149099.
(IDEC-) IDEC PHARM CORP.
                                                                                                       Homo sapiens.
EP-816498-A2.
                                                                                                                                                                                      W41568 standard; Protein; 908
W41568;
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Treating B cell lymphoma with chimeric
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   antagonists
               Human
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                                                                                                                                                                                                                                                                                                                                                               Sequence
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W09411026-A.
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MDFQVQIISFLLISASVIMSRGQIV 25
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metabotropic glutamate receptor protein - agonists an onists of which are useful to treat neurodegenerative
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57.1%;
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Pred. No. 9.6;
3; Mismatches
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CD20; peripheral blood cells;
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B cells, also
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This protein comprises a novel human metabotropic glutamate receptor, designated mGluR8. Its amino acid sequence was deduced from cDNA clones isolated from a human foetal retina cDNA library.

The metabotropic glutamate receptors are linked to mutiple second messenger pathways. They function to modulate the presynaptic release of glutamate, and the postsynaptic sensitivity of the neuronal cell to glutamate excitation. Host cells transfected with an expression vector comprising nucleic acids encoding mGluR8, are claimed. They can be used in claimed methods for evaluating the effectiveness of a test compound for the treatment or prevention of a condition associated with a deficiency or excess of stimulation of the human mGluR8 receptor. mGluR8 agonists and antagonists can be used to treat neurodegenerative diseases, or as antipsychotic, antiemetic agents.

Sequence 908 AA;
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Matches 11
751 CSLGYSILLMVTCTVYANKTRGVPETFNE
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Search completed: May 9, 2000, 21:52:05 Job time: 3757 sec

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1 MDCQLSILLLLSCS
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sp_unclassified:*
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(c) 1993 - 2000 Compugen
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Q91571 xenopus lae
Q43477 homo sapien
Q91542 homo sapien
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Q95143 homo sapien
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Q07496 gallus gall
Q07497 brachydanio
Q1737 homo sapien
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              015197 homo sapien
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5.5	5. 5	5.6	5.6	5.6	5.6	5.7	5.7	5.7	5.8	5.8	5. 8	5.9	5.9	6.0	6.1	6.1	6.5	6.6	13.3	15.0	17.1	19.1	22.7	27.1
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Q22747	,O25431	022728	016366	097702	050966	096206	015495	Q96337	023617	015718	Q18395	Q21477	032378	Q07012	065616	Q93022	023268	005989	Q91626	Q9Y1Y3	061460	057458	073875	096435
	025431 helicobacte	022728 arabidopsis		097702 canis famil		096206 plasmodium	015495 homo sapien	Q96337 brassicā na	023617 arabidopsis	015718 dictyosteli	Q18395 caenorhabdí	Q21477 caenorhabdi	032378 methylobaci	Q07012 xenopus lae	065616 arabidopsis	Q93022 homo sapien	023268 arābīdopsis	005989 staphylococ	Q91626 xenopus lae	Q9y1y3 ephydatia f	061460 caenorhabdi	057458 xenopus lae	073875 brachydanio	096435 drosophila

ALIGNMENTS

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RC TISUE-NEURAL CREST;

RX MEDLINE, 95001564.

RA WINNING R.S., SARGENT T.D.;

RY TABSEL COLOR AND ACT THE EPH family of receptor tyrosine kinase genes, has localized expression in a subset of neural crest and neural rissues in Xenopus laevis embryos.";

RI Lissues in Xenopus laevis embryos.";

RC -1- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY (BY SIMILARITY). MAY PLAY A ROLE IN THE DIFFERENTIATION OF CRANIAL COMMENTAL CREST AND OTHER TISSUES.

C -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE.

CC -1- CATALYTIC ACTIVITY: LOCALIZED EXPRESSION IN A SUBSET OF NEURAL COLORITORY: LOCALIZED EXPRESSION IN A SUBSET OF NEURAL COLORITORY: COLORITOR TRANSLENTLY IN VISCERAL ARCH 3. ALSO CENTRESSES IN THE FOREBRAIN, RHOMBOMERES R3 AND R5 OF THE HINDBRAIN C-1- SIMILARITY: CONTAINS 1 INMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC CREST. ALBACAL 1.-

CREST. ALBACAL 1.-

CREST. ALBACAL 1.-

CREST. ALBACAL 1.-

CREST. ALBACAL 1.-
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Q91694;
01-NOV-1996 (Tremblrel. 01
01-NOV-1996 (Tremblrel. 01
01-NOV-1999 (Tremblrel. 12
TYROSINE-PROTEIN KINASE RE
   Eukaryota; Metazoa; Chordata; Craniata; vercepraca,
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
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PROTEIN_KINASE_ATP; 1.
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RECEPTOR_TYR_KIN_V_1;
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TYROSINE-PROTEIN KINASE
                                                                                                                              Q91845;
Q91845;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PFAM; PF000041; fn3; 2.
PFAM; PF000069; pskinase; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF01404; EPH_lbd; 1.
SEQUENCE FROM N.A.
MEDLINE; 96125143.
XU Q., ALLDUS G., HOLDER
"Expression of truncated
                                                      Eukaryota;
Batrachia;
                                                                       Xenopus laevis (African
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transferase; Tyrosine-protein kinase; Receptor; Transmembrane; Glycoprotein;
                                             Xenopus.
                                                                                   SEK-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0014; FNTYPEIII.
                                                                                                                                                                                                                                                            147
                                                                                                                                                                                                                                                                              145
                                                                                                                                                                                    267
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                                                                                                                                                                                                                        207
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                                                                                                                                                                                                                                                                                                                                                                     Match 66.6%;
Local Similarity 70.6%;
nes 175; Conservative 7
                                                                                                                                                                                                                                                        TIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPF
|||||||||:||:||::||||::||||
TIAADESFTQVDIGDRIMKLNTEVRDVGPLSKKGFYLAFQDVGACIALVSVRVFYKKCPL
                                                                                                                                                                                                                               TVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGY
                                                                                                                                                                                                                                                                                           EEHNGGCQ
                                                                                                                                                                                                     EERGFMCQ
                                                                                                                                                                                                                       TVRNLAQFPDTITGSDTSSLVEVRGSCVDNSEEKDVPKMYCGADGEWLVPIGNCLCNAGF
                                                                                                                                                                                                                                                                                                        NWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDDDHGVKFREHQFTKID
                                                                                                                                                                                                                                                                                                                                                   PSNEVNLLDSKTIQGELGWISYP-SHGWEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PR00109; TYRKINASE.
                                                       Anura;
                                                                                                                                                                                                                                                                                                                                                                                                                 407
985
                                                                Metazoa;
                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                     271
                                                                                                                                                                                                                                                                                                                                                                                                                           1 domain.
1 20
1 985
1 547
1 547
3 569
3 325
435
533
881
108
634
108
652
745
778
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                                                     a; Chordata; Craniata; Vertebrata;
Mesobatrachia; Pipoidea; Pipidae;
                                                                Chordata; (
                                                                                                                                                                                                                                                                                                                                                                                                                   109729
                                                                                         01, Creat
01, Last
12, Last
RECEPTOR
N., WILKINSON I
Sek-1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                      39;
                                                                                                 Created)
Last sequential Last annual
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
PROTEIN KINASE
ATP (BY SIMILARITY).
BY SIMILARITY.
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                     Score 977; DB 13;
Pred. No. 2.4e-83;
9; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYS-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYROSINE-PROTEIN KINASE F
EXTRACELLULAR (POTENTIAL)
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION (AUTO-) (POTENTIAL). POTENTIAL.
                                                                     frog).
                                                                                                                                                                                                                                                                                                                                                                                                                  026BA8A5 CRC32;
                                                                                       sequence update)
annotation update)
(SEK-1 PRECURSOR (EC
                                                                                                                                       986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Signal;
tyrosine
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kinase
                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (BY
                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BY
                                                     Xenopodinae;
                                                               Amphibia;
                                                                                        2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
SIMILARITY).
disrupts
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Best Local S
Matches 175
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NP_BIND
DISULFID
BINDING
BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                               DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0109; TYRKINASE PRINTS; PRO0014; FNTYPEIII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         segmental restriction
hindbrain.";
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                                                                                                                                                                                                                                                                                                                                                                                                [mmunoglobulin
                  264
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267
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                                                                                                                                              27
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                                                                                                                                                                                 cal Similarity
175; Conser
                                                                              TVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGY
                                                                     TIAADESFTQVDIGDRIMKLNTEVRDVGPLSKKGFYLAFQDVGACIALVSVRVFYKKCPL
EEHNGGCQ
                 EERGFMCQ
                                  TVRNLAQFPDTITGSDTSSLVEVRGSCVDNSEEKDVPKMYCGADGEWLVPIGNCLCNAGF
                                                                                                                                                                                                                                                                                                                                                                                              Transmembrane;
bulin domain.
                                                                                                                                                                                                                              116
148
548
570
66
191
191
326
620
620
626
627
745
778
986
                                                                                                                                                                                 Conservative
274
                 271
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986
547
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EMBL; X91191; CAA62601.1; -...
HSSP; PO0523; 2PTK.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PFAM; PF00041; fn3; 2.
PFAM; PF000569; Pkinase; 1.
PFAM; PF000569; Pkinase; 1.
PFAM; PF01404; EPH_lbd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transferase; Tyrosine-protein kinase; Receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Development 121:4005-4016(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS. SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE I
DEVELOPMENTAL STAGE: EXPRESSION OCCURS
AT LOWER LEVELS IN R2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IDENTITY OR MOVEMENT OF CELLS.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN. BELONGS TO THE EPH FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY). REQUIRED FOR INTERACTIONS IDENTITY OR MOVEMENT OF CELLS.
                                                                        NWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDDDHGVKFREHQFTKID 144
 DWIPRSGAQRVYVEIKFTLRDCNSLPGVMGTCKETFNLYYYESNNDKERFIRETQYVKID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOR MEMBERS
                                                                                                                                                  Score 977; DE
Pred. No. 2.46
99; Mismatches
                                                                                                                                                                                                                                                                                 BY SIMILARITY.
PHOSPHORYLATION (
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
CYTOPLASMIC (POTE
IG-LIKE C2-TYPE I
                                                                                                                                                                                                                                                                                                                                                                                                              CYS-RICH.
FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                                                                          ATP (BY SIMILARITY).
BY SIMILARITY.
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                             PROTEIN KINASE.
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYROSINE-PROTEIN KINASE RECEPTOR EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                028DBBDA
                                                                                                                                                                    977; DB 13;
No. 2.4e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ဓ္ဓ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP-binding; Phosphorylation;
; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
TYPE DOMAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E EPHRIN-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN.
                                                                                                                                                  32;
                                                                                                                                                                                                                                                                                                     (AUTO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-A FAMILY (BY
REGULATE THE
                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R5
                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADP + PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AND
                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                       986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC
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                                                                                                                                                  Gaps
146
                                                                          86
                                                                                                             84
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Best Local Similarity

65.4%;

2.4e-79;

4.

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RESULT
042422
  PROSITE; PS00107; I
PROSITE; PS00109; I
PROSITE; PS00790; I
PROSITE; PS00791; I
PFAM; PF00041; fn3
MOD_RES
CARBOHYD
CARBOHYD
SEQUENCE
                                                 DOMAIN
NP_BIND
DISULFID
BINDING
ACT_SITE
                                                                                                           DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peripheral nervous system.";
Mech. Dev. 68:173-177(1997).
-!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
Neognathae; Galliformes; Phas:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TrembLrel. 05, Created)
01-JAN-1998 (TrembLrel. 05, Last sequence update)
01-NOV-1999 (TrembLrel. 12, Last annotation updat
EPH-LIKE RECEPTOR TYROSINE KINASE PRECURSOR (EC 2
                                                                                                                                                                                                                                                                       PFAM; PF00041; fn3; 2.
PFAM; PF00069; pkinase; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF01404; EPH_lbd; 1.
                                                                                                                                                                                                                                                PRINTS; PR00109; TYRKINASE. PRINTS; PR00014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  042422
                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                      Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARAUJO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-EMBRYO
                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: WITHIN THE NERVOUS SYSTEM, EXPRESSION IS
RESTRICTED TO PROSOMERES 1 AND 2 IN THE DIENCEPHALON AND ALL THE
RHOMEOMERES IN THE HINDBRAIN DURING SEGMENTATION STAGES. LATER ON,
A SUPERIMPOSED PATTERN APPEARS THAT CORRELATES WITH THE FORMATION
OF SEVERAL AXONAL TRACTS. IN THE SOUTHIC MESODERM, THE EXPRESSION
CORRELATES WITH SEGMENTATION AND THE GUIDANCE OF BOTH NEURAL CREST
AND MOTOR AXONS THROUGH THE SCLEROTOMES.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALLYTIC
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAIN.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYROSINE PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression of chick EphA7
                                                                                                                                                                                                                                                                                                                                                                          Y14271; CAA74643.1; -. P00523; 2PTK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98092111.
                                                                                                                                                                                                                         Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                      Tyrosine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N.A.
                                                                                                                                                                                                                                                              TYRKINASE.
                                                                                                                                                                                                                                                                                                                       PROTEIN_KINASE_ATP; 1.
PROTEIN_KINASE_TYR; 1.
RECEPTOR_TYR_KIN_V_1;
RECEPTOR_TYR_KIN_V_2;
                         CEPHA7).
                                                                                                                                                                                                          Glycoprotein;
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phasianidae;
 ₹,
                     FIBRONECTIN TYPE-III (BY FIBRONECTIN TYPE-III (BY PROTEIN KINASE. ATP (BY SIMILARITY). BY SIMILARITY. ATP (BY SIMILARITY). BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. BY SIMILARITY. PHOSPHOXYLATION (AUTO-) (POTENTIAL.
                                                                                                                                            CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
POTENTIAL.
1; 6B6BFD17
                                                                                                                                   IG-LIKE C2-TYPE CYS-RICH.
                                                                                                                                                                                  EPH-LIKE RECEPTOR TYROSINE EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                      kinase; ATP-binding; Phosphorylation; oprotein; Signal; Immunoglobulin domai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; ianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             during
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                                                                                                           78)
78)
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                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the
                                                                                                           SIMILARITY).
SIMILARITY).
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                                                                                                                                                                                                KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             central
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Query

63

Score

934.5;

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Length

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RESULT
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                              ZFIN, ZDB-GENE-990415-58; Zekl.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; FALSE_NEG.

PFAM; PF00069; Pkinase; 1.

PFAM; PF00536; SAM; 1.

PFAM; PF01404; EPH_1bd; 1.

R PFAM; PF01404; FMTYPEIII.

R PFAMS; PR00109; TYRKINASE.

R PRINTS; PR00014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       013146;
              Transferase;
Receptor; Tra
                                                                                                                                                                                                                                                                         - -
                                                                                                                                                                                                                                                                                                                                                  developing zebrafish nervous system. Dev. Dyn. 209:166-181(1997).
-!- FUNCTION: RECEPTOR FOR MEMBERS (
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Neopterygil; Teleostei; Buteleostei; Ostariophysi; (
Cyprinoidea; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUL-1997 (Tremblrel. 04,
01-JUL-1997 (Tremblrel. 04,
01-NOV-1999 (Tremblrel. 12,
EPH-LIKE KINASE 1 PRECURSOR
                                                                                                                                                                                                           ++
                                                                                                                                                                                                                                                                                                                                                                                                        BOVENKAMP D.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                              Novel Eph-family receptor tyrosine kinase developing zebrafish nervous system.";
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                                                                                                                                                                                                        SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATAL DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY. SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN. SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION: TYPE TISSUE SPECIFICITY: WIDELY
                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: ATP
                                                                                                                                                                                                                                                            NERVOUS SYSTEM.
                                                                                                                                                                                                                                                                                                 TYROSINE PHOSPHATE
                                                                                                                                                                                                                                                                                                                           SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYM 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLSCSV----LDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDEHYTPI
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 Transmembrane;
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Tyrosine-protein kinase; ATP-binding; Phosphorylation; ansmembrane; Glycoprotein; Signal; Immunoglobulin domai 1 20 BY SIMILARITY.
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P.;
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Last annotation update)
(EC 2.7.1.112) (TYROSINE-PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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3; Mismatches
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                                                                                                                                                                                                                                                                      E PROTEIN.
IN THE DEVELOPING ZEBRAFISH
                                                                                                                                                                                                                                                                                                                                      EPHRIN-B FAMILY. MAY
N THE DEVELOPING NERVO
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Cypriniformes;
                                                                                                                                                                                                                                               CATALYTIC
                                                                                                                                                                                                                                                                                                             PROTEIN
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Best Local Sin
Matches 156;
                                                                                                                                                                                                                                                                073879
O73879;
O73879;
O73879;
O1-AUG-1998 (TrEMBLrel. 07, Created)
O1-AUG-1998 (TrEMBLrel. 07, Last sequence update)
O1-NOV-1999 (TrEMBLrel. 12, Last annotation update)
EPH-LIKE RECEPTOR TYROSINE KINASE RTK4 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NP_BIND
DISULFID
BINDING
BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
CARBOHYD
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VARIANT
SEQUENCE
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DOMAIN
TRANSMEM
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DOMAIN
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DOMAIN
COOKE J.E., XU Q., WILSON S.W., HOLDER N
Dev. Genes Evol. 206:515-531(1997).
EMBL; AJ005339: CAA06303:1; -.
HSSP; P00523; 2PTK.
FIN: ZDB-GENE-990415-61; rtk4.
PROSITE; PS00791; RECEPTOR TYR KIN_V_2;
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                             Submitted
                                                                                                                                                                                COOKE
                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                               Cyprinoidea; Cyprinidae;
                                                                                                                                                                                                                                                 Neopterygii;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TEGEWLVPIGKCSCNAGYEERGFMCQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADGGWLVPIGRCVCRPGFEEVDGHCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDHGV----KFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                             (MAR-1998)
                                                                                                                                                                                                                                          o rerio (Zebrafish) (Zebra dan
Metazoa; Chordata; Craniata;
1; Teleostel; Euteleostel; Ost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                 Rasborinae;
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IG-LIKE C2-TYPE DOMAIN.
CYS-RICH.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY.
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 851.5;
Pred. No. 1.4e
14; Mismatches
                                                                                                                                                            EMBL/GenBank/DDBJ
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POTENTIAL.
POTENTIAL.
POTENTIAL.
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                                                                                                                                                                                                                             ata; Vertebrata;
; Ostariophysi; C:
; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; DB 13;
1.4e-71;
hes 57;
                                                                                                                                                            databases
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Best Local S
Matches 149
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PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PFAM; PF001404; EPH_lbd; 1.
PFAM; PF00069; pkinase; 1.
PFAM; PF00041; fn3; 2.
NON_TER 1 1
NON_TER 880 880
SEQUENCE 880 AA; 98862 MW; 7C139606 CR
                                                                                                                                                                                                                                                                       JONES T.L., KARAVANOVA I., MAENO M., ONG R.C., KUNG H.-F., "EXPRESSION OF AN AMPHIBIAN homolog of the Eph family of retyrosine kinases is developmentally regulated."; Oncogene 10:1111-1117(1995).

-- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-B FAMILY.
-- FUNCTION: RECEPTOR FOR MEMBERS OF THE CENTRAL NERV.
-- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PRITYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TIEMBLIEL 01.
01-NOV-1996 (TIEMBLIEL 01.
01-NOV-1999 (TIEMBLIEL 12.
EPHRIN TYPE-B RECEPTOR XEK
KINASE RECEPTOR XEK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q91571
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBU
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN
EMBL; U14164; AAA74888.1; -.
HSSP; P00523; 2PTK.
HRSSP; P00523; 2PTK.
PROSITE; PS001043; GRAM_POS_ANCHORING;
PROSITE; PS00109; PROTEIN_KINASE_ATP;
PROSITE; PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
Batrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    XEK.
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE; 95215070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q91571;
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                                                                          DEVELULIAR LOCATION: TYPE I MEMBRANE PROTEIN.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

DEVELOPMENTAL STAGE: MATERNALLY EXPRESSED, IT DECREASES AT MID DEVELOPMENTAL STAGE: MATERIOR AND LATE NEURULATION. EXPRESSED AT HIGHER LEVELS IN THE ANTERIOR AND DORSAL REGIONS OF EMBRYONIC STACES 16, 24 AND 37. IN ADULT IT APPEARS TO BE UBIQUITOUSLY EXPRESSED WITH HIGHER EXPRESSION IN BRAIN AND OVARY. EXPRESSION I THE BRAIN, BRACHIAL ARCHES, TRIGEMINAL FACIAL GANGLION, AND THE EMPAIN OF SWIMMING TADPOLE STAGE OF DEVELOPMENT.

SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EMPHRIN RECEPTOR FAMILY.

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSRAGFYLAFQDVGACIALVSVHVFYKKCPLAVRNLAQFPDTVTGADTSSLVEVRGSCVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCVN
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149; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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68.0%;
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, Last annotation update)
PRECURSOR (EC 2.7.1.112)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 838.5;
Pred. No. 2.1e
36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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                                 UNKNOWN_1
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.es 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amphibia;
Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                        MILY. MAY PLAY A
L NERVOUS SYSTEM.
P + PROTETM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 143; Conserv
                                                                                                                                      043477 PRELIMINARY;
043477;
01-JUN-1998 (Tremblrel. 0
01-JUN-1998 (Tremblrel. 0
01-NOV-1999 (Tremblrel. 1
PROTEIN-TYROSINE KINASE E
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SEQUENCE
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PFAM; PF00069; PFAM; PF00536;
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DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor;
SIGNAL
                                                                                          Homo sapier
Eukaryota;
SEQUENCE FROM N.A.
MEDLINE; 96154673.
IKEGAKI N., TANG X.X.,
SULMAN E.P., BRODEUR G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE;
                                                                                                                              EPHB2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF01404; EPH_lbd; 1. PRINTS; PR00109; TYRKINASE.
                                                                               Eutheria;
                                                                                                                                                                                                                                                                                                      236
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                                                                            sapiens (Human).
ryota; Metazoa; C
meria; Primates; C
                                                                                                                                                                                                                                                                                               YYETDSNIENKISTFWNESPYLKVDTIAADESFSQVDFGGRLMKVNTEVRSEGPLTRSGF
                                                                                                                                                                                                                                                                                                                                                                                                                                         YMESDDDHGVK----FREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIRTYQVCNVFGPKQNNWLLTTFIPRRGAHRVYVEMRFTVRDCSSLPNVPGSCKETFNLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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745
779
336
428
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; pkinase; 1.
; SAM; 1.
; EPH_lbd; 1.
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RECEPTOR_TYR_KIN_V_2;
                                                                            Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.4%;
.M.,
                                                                                                                                          06, Created)
06, Last sequence update)
12, Last annotation updat
EPHB2V.
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 X.G., BIEGEL J
PLEASURE D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 768.5; 1
Pred. No. 8.9e
55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
CYS-RICH.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROTEIN KINASE.
ATP (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
PHOSPHORYLARITON (AUTO-) (POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
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                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                      1055
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.9e-64;
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                Α.,
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                ALLEN
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                c:,
                                                                                            Mammalia
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                YOSHIOKA
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Best Local Sin
Matches 138;
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Submitted (SEP-1997) to the EMBL/GenBank/DI
EMBL; AF025304; AAB94602.1; -.
HSSP; P00523; 2PTK.
PROSITE; PS007109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PFAM; PF00041; fn3; 2.
PFAM; PF00069; pkinase; 1.
PFAM; PF000536; SAM; 1.
PRINTS; PR001014; FNTYPEIII.
STEIN E., SCHOECKLMANN H.O., STEIN E., SCHOECKLMANN H.O., ENDIT THE EMBL; AF037333; AAB94628.1; -EMBL; AF037334; AAB94628.1; -EMBL; AF037334; AAB94628.1; -HSSP; P08631; 2HCK.
PFAM; PF000641; fn3; 2.
PFAM; PF00069; PKINASE; 2.
PFAM; PF00536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      043569 PRELIMINARY; PRT; 943 AA.
043569; 01-JUN-1998 (TIEMBLIEL. 06, Created)
01-JUN-1998 (TIEMBLIEL. 06, Last sequence update)
01-NOV-1999 (TIEMBLIEL. 12, Last annotation updat)
EPH-LIKE RECEPTOR TYROSINE KINASE HEPHBLO

[EPH-LIKE RECEPTOR TYROSINE KINASE HEPHBLD).
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                                                                                                                                                                                                                                                                         SEQUENCE FROM
TISSUE-KIDNEY
                                                                                                                                                                                                                                                                                                                                                                          Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wolecular characterization and chromosomal localization of DRT (EPHT3): a developmentally regulated human protein-tyrosine kinase yene of the EPH family "; um. Mol. Genet. 4:2033-2045(1995).
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                                                                                                                                                                                                                                                                                                                                                                   sapiens (Human).
ryota; Metazoa; Chordata; Craniata; Vertebrata;
eria; Primates; Catarrhini; Hominidae; Homo.
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ne EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 767; DB
Pred. No. 1.3e
52; Mismatches
                                                                                                                                                                                                        EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                       DANIEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EAF28155 CRC32;
                                                                                                                                                                                                                                   T.O.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
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                                                                                                                                                                                                           databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia;
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Best Local S
Matches 138
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01-MAY-1999
01-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                     Receptor;
SEQUENCE
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PRINTS; PR00109; TYKINASE.
PRINTS; PR00014; ENTYPEIII.
SEQUENCE 943 AA; 105291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-KIDNEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EPH-LIKE
                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00107; PROTEIN_KINASE_ATP; PROSITE; PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177
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                                                                                                                                                                                                                                                  Local Similarity
les 138; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match
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                                                                                                                                                                                                 7 ILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDEHYTPIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              c-Jun Kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol.
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                                                                           TYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLLLESAV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDDDHGVK----FREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLA
TDSVIATKKSAFWSEAPYLKVDTIAADESFSQVDFRGRLMKVNTEVRSFGPLTRNGFY
                                    SDDDHGVK----FREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E., HUYNH-DO U., L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FQDYGACMILLSVRVFFKKCPSIVQNFAVFPETMTGAESTSLVIARGTCIPNAEEVDVPI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYQVCNVFEPNQNNWLLTTFINRRGAHRIYSEMRFTVRDCSSLPNVPGSCKETFNLYYYE
                                                                                                                                                                                                                                                                                                                                                                                                                                ol. Chem. 0:0-0(1997).
AF037331; AAD02030.1; -.
P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138;
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                                                                                                                                                                                                                                                                                                                                                                          Kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Metazoa;
                                                                                                                                                                                                                                                                                                                                                       984 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TIEMBLrel. 10, Created)
(TIEMBLrel. 10, Last sequence up
(TIEMBLrel. 12, Last annotation
CEPTOR TYROSINE KINASE HEPHB1.
                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Human).
etazoa; Chordata; Craniata; Vertebrata; Mammalia;
etazos; Catarrhini; Hominidae; Homo.
                                                                                                                                                              -----AAMEETLMDTRTATAELGWTANPASGWEEVSGYDENLNTIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----AAMEETLMDTRTATAELGWTANPASGWEEVSGYDENLNTIR
                                                                                                                                                                                                                                                                                                                                                     110041 MW;
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                                                                                                                                                                                                                                                                   50.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LANE A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor,
                                                                                                                                                                                                                                                  53;
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                                                                                                                                                                                                                                              Score 739.5; DB 4
Pred. No. 4.7e-61;
3; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 739.5; DB 4;
Pred. No. 4.4e-61;
3; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                     DF5C8ED3 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CERRETTI D.P., DANIEL r, EphB1/ELK, couples 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C4C78A21 CRC32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             984
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                                                                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activation
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                      182
                                                                                                                   126
                                                                                                                                                              56
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                                                                                                                                                                                                       PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PFAM; PF00041; fn3; 2.
PFAM; PF00069; PAINASE; 1.
PFAM; PF00536; SAM; 1.
PFAM; PF001404; EPH_1bd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q91735
Q91735;
NP_BIND
DISULFID
BINDING
ACT_SITE
MOD_RES
                                                                                                                                                    Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
Batrachia;
                                                    DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Novel members of the eph receptor t during Xenopus development."; Oncogene 11:1745-1752(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TremBLrel. 01, Last sequence update)
01-NOV-1999 (TremBLrel. 12, Last annotation update)
EPHRIN TYPE-B RECEPTOR PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. MEDLINE; 96068901. SCALES J.B., WINNI
                                                                                                                               DOMAIN
                                                                                                                                                                                    PRINTS; PRO00109; TYRKINASE. PRINTS; PRO0014; FNTYPEIII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996
                                                                                                                     TRANSMEM
                                                                                                                                                                          Transferase; Tyrosine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183
                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
TISSUE SPECIFICITY: EXCRESSED IN THE EMBRYO II PRE-SOMITIC
MESODERM, CAUDAL SOMITES, MIDBRAIN, AND CEMENT GLAND. MOST
ABUNDANT IN ADULT BRAIN, EYE, HEART, LUNG AND OVARY. LOWER
IN INTESTINE, KIDNEY, OVIDUCT AND PHARYNX.
DEVELOPMENTAL STAGE: EXPRESSED DURING EARLY DEVELOPMENT.
SIMILARITY: TO OTHER PROTEIN TYROSINE KIALY DEVELOPMENT.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: RECEPTOR SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P00523; 2PTK.
                                                                                                                                                                                                                                                                                                        L43620; AAA93526.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RECEPTOR) (TCK)
                                                                                                                                                               Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Metazoa; Chordata; Craniata; Vertebrata;
Anura; Mesobatrachia; Pipoidea; Pipidae;
  535
536
536
178
178
316
424
609
615
734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
  16
974
534
974
102
315
315
423
520
623
623
734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12,
                                                                                                                                                    Glycoprotein;
POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
          ATP (BY SIMILA
BY SIMILARITY.
ATP (BY SIMILA
BY SIMILARITY.
                                        PROTEIN KINASE.
ATP (BY SIMILARITY).
                                                               FIBRONECTIN TYPE-III.
                                                                                                         CYTOPLASMIC
                                                                                                                            EPHRIN TYPE-B RECEPTOR.
EXTRACELLULAR (POTENTIAL)
                                                                                      CYS-RICH
PHOSPHORYLATION (AUTO-) (POTENTIAL).
                                                                                               IG-LIKE
                                                                                                                                                              kinase; ATP-binding; Phosphorylation
oprotein; Signal; Immunoglobulin doma
                     (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C.S., SHEA L.J.,
tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                           OF THE
                                                                                               C2-TYPE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        974
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                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPHRIN-B
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subfamily expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                      ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amphibia;
Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                 CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN
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RESULT
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Best Local S
Matches 129
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Best Local Similarity
Matches 134; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (NOV-1997) to the EMBL/GenB
EMBL; AE037332; AE03231.1; -
HSSP; P00523; 2PTK.
PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               095143;
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
EPH-LIKE RECEPTOR TYROSINE KINASE HEPHB1B.
                                                                                                                                                                                                                                                                                                                                                                                                          Receptor; Kinase. SEQUENCE 973 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-KIDNEY;
STEIN E., SCHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A.
                         217
                                                                140
                                                                                                      157
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                                                                                                                                                                                                                                          ELGWISYPSHGWEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELK
ELGWTANPASGWEEVSGYDENLNTIRTYQVCNVFEPNQNNWLLTTFINRRGAHRIYSEMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKLYCNGDGDWMVPVGACTCAAGFEPAGKDTQCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -RMYCSTEGEWLVPIGKCSCNAGYEERG--FMCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESDDDHGVK----FREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDEHYTPI
                                                          FRGRIMKVNTEVRSFGPLTRNGFYLAFQDYGACMILLSVRVFFKKCPSIVQNFAVFPETM
                                                                                 LGDRILKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AFQDLGACVSLISVRVFFKKCPRTTAGFASFPETITGAEPTSLVIAPGTCVPNALEVSVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESDSDSASADSPFWMENPYIKVDTIAPDESFSRRDSG----RVNTKIRSFGPISRAGFYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVFVILALSAVQGL-----EETLMDTKWTTSELAWVAYPDSGWEEVSGYDEASNPI
                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SCHOECKLMANN H.O., (NOV-1997) to the
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420
974 i
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108263
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Pred. No. 1.2e
51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                          Score 713.5; DB 4
Pred. No. 1.3e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
POTENTIAL.
W; BD419F6D CRC32;
                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                         Length
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RESULT
Q07494
ID Q0
AC QC
DT Q1
DT 01
DT 01
DT C1
GN C1
GN G1
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Best Local Similarity
Matches 122; Conserv
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HSSP; P00523; 2PTK.
PROSITE; PS00790; RECEPTOR_
PROSITE; PS00791; RECEPTOR_
PROSITE; PS00109; PROTEIN_K
PROSITE; PS00107; PROTEIN_K
PROSITE; PS00107; PROTEIN_K
PRAM; PF01404; EPH_1bd; 1.
PFAM; PF00041; fn3; 2.
PFAM; PF000526; SAM; 1.
                                                              Q07494;
Q07494;
Q1-NOV-1996
Q1-NOV-1996
Q1-NOV-1999
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Q07498;
Q1-NOV-1996
                                          CEK6
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
---**--- Galliformes; Phasianidae; Phasianinae; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TIEMBLIEL. 01, Created)
01-NOV-1996 (TIEMBLIEL. 01, Last sequence update)
01-NOV-1999 (TIEMBLIEL. 12, Last annotation update)
TYROSINE KINASE CEKIO RECEPTOR (EC 2.7.1.112) (FRAGMENT).
    Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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Oncogene 8:1807-1813(1993)
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NON_TER
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SAJJADI F.G., PASC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-EMBRYO;
MEDLINE; 93288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFAM;
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M; PF00361; SAM; 1.
M; PF00069; Pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IQGELGWISYPSHGWEEISGVDEHYTPIRTYQVCNYMDHSQNNWLRTNWVPRNSAQKIYV
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VTSELAWTTHPETGWEEVSGYDEAMNPIRTYQVCNVREANQNNWLRTKFIQRQDVQRVYV
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                                                                                                                                                                                                                                                                                                                                                                   PROTEIN (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          QMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELKFTLRDCNSIPLVLGTCKETFNLYYMESDDD----HGVKFREHQFTKIDTIAADESFT 153
                                                                                                                                                                                                                                                                                                                                             ETLTGAEPTSLVIAPGTCIPNAVEVSVPLKLYCNGDGEWMVPVGACTCAAGYEPAMKDTQ
  gallus (Chicken)
                                                                                                                                                                                                                                                            257
                                                                                                                                                                                                                                                                                                       271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FROM N.A.
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                                                              (TrEMBLrel.) (TrEMBLrel.)
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                                                                                                                                                   PRELIMINARY;
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RECEPTOR_TYR_KIN_V_2;
PROTEIN_KINASE_TYR; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     109578
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01,
12,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 679; DB 13;
Pred. No. 2.2e-55;
1; Mismatches 57
                                                                                                                                                   PRT;
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                                                            sequence u
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Best Local Sim
Matches 112;
Mech. Dev. 48:153-164(1994).

EMBL; U11493; AAA67925.1; -.

HSSP; P00523; ZPTK.

MGD; MGI:104770; Ephb3.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                              Q60669;
Q60669;
01-NOV-1996
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; M
Neognathae;
[1]
                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Entheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P00523; 2PTK.

PROSITE; PS00107; PROTEIN_KINASE_ATP;
PROSITE; PS00109; PROTEIN_KINASE_TYR;
PFAM; PF00536; SAM; 1.

PFAM; PF00069; pkinase; 1.

PFAM; PF01404; EPH_lbd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE, 93288394.
SAJJADI F.G., PASQUALE E.B.;
"Five novel avian Eph-related
expressed.";
                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE; 95200798.
                                                                                                                                                                                                                                                                                                                                                                        EPHB3 OR ETK2.
                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1999 (TrEMBLrel. 12, PROTEIN KINASE (FRAGMENT).
                                                                                                                                                    "Identification of novel protein of the developing mouse heart."; Mech. Dev. 48:153-164(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDDDHGVK----FREHQFTKIDTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LMDTRTATAELGWTANPPSGWEEVSGYDENLNTIRTYQVCNVFEPNQNNWLLTTFINRRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENNVACR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AHRIYTEMRETVRDCSSLPNVPGSCKETFNLYYYETDSVIATKKSAFWTEAPYLKVDTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        z19110;
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9110; CAA79526.1; -.
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; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                                    CONLON F.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; SAM; 1.
; pkinase; 1.
; EPH_lbd; 1.
; fn3; 2.
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                                                                                                                                                                                                                    ROBERTSON E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43;
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Pred. No. 1.8e
43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation updat
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hes 53;
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Mus.
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Best Local Similarity
Matches 108; Conser
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Q91736;
Q1-NOV-1996
Q1-NOV-1996
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PFAM; PFO
PFAM; PFO
NON_TER
SEQUENCE
             EMBL; L43
HSSP; P00
PROSITE;
PROSITE;
PROSITE;
PROSITE;
PRAM; PF0
PFAM; PF0
PFAM; PF0
PFAM; PF0
                                                                                                                                  --- SUBCELLULAR COCATION: TYPE I MEMBRANE PROTEIN.
--- TISSUE SPECIFICITY: EXPRESSED IN THE EMBRYO IN THE BRAIN
--- FISSUE SPECIFICITY: EXPRESSED IN THE EMBRYO IN THE BRAIN
--- SPINAL CORD AND IN THE FIRST AND FOURTH VISCERAL ARCHES.
--- ABUNDANT IN ADULT BRAIN, WITH LOWER LEVELS IN EYE, HEART,
--- OVIDUCT, LUNG AND PHARYINX.
--- OVIDUCT, LUNG AND PHARYINX.
--- IDBYELOPMENTAL STAGE: EXPRESSED DURING EARLY DEVELOPMENT.
--- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATA
--- DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
--- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
--- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1996 (TIEMBLIEL. 01, Created)
01-NOV-1996 (TIEMBLIEL. 01, Last sequence update)
01-NOV-1999 (TIEMBLIEL. 12, Last annotation update
EPH RECEPTOR TYROSHIE KINASE (XELK) (FRAGMENT).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrat;
Batrachia; Anura; Mesobatrachia; Pipoidea; Pipida
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE; 96068901.
SCALES J.B., WINNING R.S., RENAUD C
"Novel members of the eph receptor
during Xenopus development.";
Oncogene 11:1745-1752(1995).
                                                                                                                                                                                                                                                                    -I- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -
TYROSINE PHOSPHATE.
 Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                        Xenopus.
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          SITE; PS00107; PROTEIN_KINASE_ATP; 1.
SITE; PS00109; PROTEIN_KINASE_TYR; 1.
SITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
SITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
M; PF000041; fn3; 2.
M; PF000041; fn3; 2.
M; PF00069; pkinase; 1.
M; PF000536; SAM; 1.
M; PF000536; SAM; 1.
                                                                                                                                                                                                                                                                                              SIMILARITY).
                                                                                                                                                                                                                                                                                                        FUNCTION: RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCVNNSKEEDPP-RMYCSTEGEWLVPIGKCSCNAGYE 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACIANAVEVSVPLKLYCNGDGEWMVPVGACTCATGHE 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRG
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PF00036;
PF00069;
                                                                                                                L43621; AAA93527.1;
P00523; 2PTK.
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Tyrosine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPH_lbd;
fn3; 2.
SAM; 1.
pkinase;
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ea; Pipidae;
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ATP (BY SIMILARITY).
BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (POTENTIAL).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 563.5; DB 13; Length 902; Pred. No. 1.4e-44; 2; Mismatches 34; Indels 7;
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7; C096D006 CRC32;
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CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN (BY SIMILARITY).
CYS-RICH.
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OM protein - protein search, using sw model
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Run on: May 9, 2000, 22:32:11; Search time 49:21 Seconds (without alignments) 167.716 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-104-340-4
1466
1 MDCQLSILLLISCSVLDSFG......VPIGKCSCNAGYEERGFMCQ 271

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 83857 segs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database : SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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MBL; M83941; AAA58633.1; MBL; A28003; CAA01906.1; IR; A38224; A38224. SSP; P00523; 2PTK. IM; 179611; IM; 179611; IM; PR001014; FNITYPEIII. RINTS; PR001019; TYRKINASE. ROSITE; PS00107; PROTEIN_KINASE_ATP; 1. ROSITE; PS00109; PROTEIN_KINASE_TYR; 1. ROSITE; PS00109; PROTEIN_KINASE_DOM; 1.	his SWISS-PROT entry is copyright. It is produced through a collaborati etween the SWISS Institute of Bioinformatics and the EMBL outstation he European Bioinformatics Institute. There are no restrictions on i se by non-profit institutions as long as its content is in no wodified and this statement is not removed. Usage by and for commerci ntities requires a license agreement (See http://www.isb-sib.ch/announcr send an email to license@isb-sib.ch).	-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN TYROSINE PHOSPHATE!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN!- TISSUE SPECIFICITY: RESTRICTED TO LYMPHOID TUWOR CELL LINES!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELOWGS TO THE EPHRIN RECEPTOR FAMILY!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.	EQUENCE OF 21-29 AND 840-860, AND CHARACTERIZATION EQUENCE OF 21-29 AND 840-860, AND CHARACTERIZATION COUNTY OF THE PRINT OF A COULD PLAY A ROLE FUNCTION. EQUIN RECEPTOR FOR MEMBERS OF THE EPHRIN-A2, -A3, -A4 AND -A5. COULD PLAY A ROLE FUNCTION.	[1] SEQUENCE FROM N.A. MEDLINE; 92179233. MILKS I.P., Wilkinson D., Salvaris E., Boyd A.W.; Wicks I.P., Wilkinson D., Salvaris E., Boyd A.W.; "Molecular cloning of HEK, the gene encoding a receptor tyrosine kinase expressed by human lymphoid tumor cell lines."; Proc. Natl. Acad. Sci. U.S.A. 89:1611-1615(1992).	01-DEC-1992 (Rel. 24, Created) 01-DEC-1992 (Rel. 24, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) 01-NOV-1997 (Rel. 35, Last annotation update) EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR ETK1) (HEK). EPHA3 OR ETK1 OR ETK OR HEK. HOMO Sapiens (Human). Eukharyota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	LT 1 HUMAN EPA3_HUMAN STANDARD; PRT; 983 AA. P29320:

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PROSITE; PS00791; RECEPTOR_TYR_KIN_\
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PFAM; PF00041; fn3; 2.
PFAM; PF00069; pkinase; 1.
PFAM; PF00536; SAM; 1.
                                 Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Entheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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01-DEC-1992 (Rel. 24, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC
KINASE RECEPTOR ETK1) (MEK4).
EPHA3 OR ETK1 OR MEK4 OR TYRO4.
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STRAIN-ICR
                SEQUENCE FROM N.A.
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RECEPTOR_TYR_KIN_V_2;
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ATP (BY SIMILARITY).

BY SIMILARITY.

BY SIMILARITY.

POSPHORYLATION (AUTO-) (BY SIMILARITY).

POTENTIAL.

POTENTIAL
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TISSUE-EMBRYO
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Pred. No. 3.1
0; Mismatches
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CYS-RICH.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPHRIN TYPE-A RECEPTOR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kinase; ATP-binding; Phosphorylation;
pprotein; Signal.
                                                                                                                                                                                                                                 PRT;
                                                                                                                                        ion update)
(EC 2.7.1.112)
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1.1e-122;
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R PRINTS; PRO0109; TYRKINASE_ATP; 1.

R PRINTS; PR00109; TYRKINASE_ATP; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

R PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS00199; RECEPTOR_TYR_KIN_V_1; 1.

R PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

R PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

R PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

R PROSITE; PS001186; EGF_2; UNKNOWN_1.

R PROM; PF00041; fina; 2.

R PRAM; PF00099; pkinase; 1.

R PFAM; PF00099; pkinase; 1.

R PFAM; PF00536; SAM; 1.

R PFAM; PF01404; EPH_Lbd; 1.

R PFAM; PF01404
  Query Match
Best Local Similarity
Matches 260; Conserv
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Sajjadi F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M68513; AAA39521.1; -.
EMBL; M68515; AAA39522.1; ALT_SEQ.
PIR; A45583; A45583.
HSSP; P16109; 1FSB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at least two forms of the receptor.";

New Biol. 3:769-778(1991).

-i- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A
EPHRIN-A2, -A3, -A4 AND -A5.

-i- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Identification of a new eph-related receptor tyrosine kinase gene from mouse and chicken that is developmentally regulated and encoder."
                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:99612; EPHA3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OF THE SAME GENE.
TISSUE SPECIFICITY: GREATEST LEVELS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN TYROSINE PHOSPHATE.
SUBCELULAR LOCATION: TYPE I MEMBRANE PROTEIN.
ALTERNATIVE PRODUCTS: A SECRETED VARIANT WITHOUT THE TRANSMEMBRANE REGION AND THE KINASE DOMAIN IS PRODUCED BY ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92031278
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Score 1400.5; DE Pred. No. 2e-116; 3; Mismatches
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ATP (BY
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                                                                                                                                                                                                PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
POTENTIAL.
POTENTIAL.
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POTENTIAL.
                                                                                                                                        MISSING (IN SHORT ISOFORM)
BE44A6655D8107A2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FIBRONECTIN TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL). CYS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPHRIN TYPE-A RECEPTOR 3. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                               ATP
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                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KINASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A LIYY, MCTIETRAN C.F., Feldman A.M.;

I I-1 beta alters the expression of the receptor tyrosine kinase T r-EphA3 in neonatal rat cardiomyocytes.";

L Am. J. physiol. 274:H331-H341(1998).

C -!- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS C EPHRIN-A2, -A3, -A4 AND -A5.

C -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + ROTEIN TYROSINE PHOSPHATE.

C -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

C -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
PRINTS; PRO0014; FNTYPEIII.

PRINTS; PRO0109; TYRKINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

PFAM; PF00041; fn3; 2.

PFAM; PF00069; pkinase; 1.

PFAM; PF00059; SAM; 1.

PFAM; PF001404; EPH_1bd; 1.
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01-NOV-1997 (Rel. 35, La
15-FEB-2000 (Rel. 39, La
EPHRIN TYPE-A RECEPTOR 3
KINASE RECEPTOR REK4).
                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sor send an email to license@isb-sib.ch).
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HSSP; P16109;
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Sciurognathi; Murida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Created)
, Last sequence
, Last annotation 3 PRECURSOR
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annotation
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; 2.7.1.112)
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ae; Murinae;
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Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       restrictions
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MBL outstation -
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Best Local S
Matches 258
SEQUENCE FROM N.A.

MEDLINE; 9203178.

Sajjadi F.G., Pasquale E.B., Subramani S.;

"Identification of a new eph-related receptor tyrifrom mouse and chicken that is developmentally relationation of the receptor.";

at least two forms of the receptor.";

New Biol. 3:769-778(1991).

-IPHRIN-12, A3, A4 AND -A5.

-IPHRIN-2, A3, A4 AND -A5.

-IPHRIN-12, A3, A3, ATP + A PROTEIN TYROSINE PROTEIN TYROSINE PROTEIN TYROSINE PROTEIN TYROSINE
                                                                                                                 P29318;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence updat
01-NOV-1997 (Rel. 35, Last annotation upd
EPHRIN TYPE-A RECEPTOR 3 PRECURSOR (EC 2.
KINASE RECEPTOR ETK1) (CEK4).
EPHA3 OR ETK1 OR CEK4.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; V
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DOMAIN
NP_BIND
BINDING
BINDING
ACT_SITE
MOD_RES
CARBOHYD
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SIGNAL
CHAIN
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DOMAIN
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Receptor; Tran
                                                                                                           Neognathae;
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                                                                                                                                                                                                                                           RMYCSTEGEWLVPIGKCTCNAGYEERGFICQ
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                                                                                                         Galliformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 95
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                                                                                                         lata; Craniata; Vertebrata;
Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein;
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POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1399; I
Pred. No. 2.7e
3; Mismatches
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V; F170C49312F7A0AB
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CYS-RICH.
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C 2.7.1.112) (TYROSINE-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal.
           TYROSINE
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.7e-116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE-III.
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                            EPHRIN-A
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                                                    tyrosine kinase
y regulated and (
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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                            FAMILY.
                                                                                                         ; Archosauria; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Phosphorylation;
           ΑĐΡ
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encodes
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Best Local
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PROSITE; PSO0109; PROTEIN_KINASE_TYR; 1.

PROSITE; PSO0109; PROTEIN_KINASE_DOM; 1.

PROSITE; PSO0799; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

PFAM; PF00069; pkinase; 1.

PFAM; PF00053; SAM; 1.

PFAM; PF011404; EPH_1bd; 1.
                                                                                                                                                                                                                                                                 NP_BIND
BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0014; FNTYPEIII. PRINTS; PRO0109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
-1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M68514; AAA48666.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transferase; Tyrosine-protein
  188
                          189
                                                    128
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SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: TYPE I
TISSUE SPECIFICITY: GREATEST
                                                                                                                                                                LLLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDEHYTPIRTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              в45583; в45583.
          CVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCVNNSKEEDPPRMYCSTEG
                                                              DDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGFVNKKGFYLAFQDVGA
                                                                                                              QVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESD
                                                                                                 QESNVMDHSQNNWLRTNWIPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESD
                                                                                                                                                   LLLLCAALGSAGRLSARPGNEVNLLDSKTIQGELGWISYPSHGWEEISGVDEHYTPIRTY
CVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCVNHSKEEEPPKMYCSTEG
                                                 DDHLAKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEVREVGPVSKKGFYLAFQDVGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P00523;
                                                                                                                                                                                                                Similarity
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91.6%;
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CYTOPLASMIC
CYS-RICH.
                                                                                                                                                                                                               Score 1309;
Pred. No. 2
                                                                                                                                                                                                                                                                                        POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                           ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                         FIBRONECTIN TYPE-III. FIBRONECTIN TYPE-III. PROTEIN KINASE.
                                                                                                                                                                                                                                                              POTENTIAL.
; E8895F0BDF77651E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPHRIN TYPE-A RECEPTOR 3. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                     Mismatches
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LEVELS OF EXPRESSION OCCURRING
                                                                                                                                                                                                               .6e-1
                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
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                                                                                                                                                                                                                           Length
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247
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Best Local S
Matches 180
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PRINTS; PR00014; ENTYPEIII.

PRINTS; PR00109; TYRKINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS001186; EGF_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                        DOMAIN
NP_BIND
BINDING
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CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P54758:
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
EPHRIN TYPE-A RECEPTOR 6 PRECURSOR (EC 2.7.1.1
KINASE RECEPTOR EHK-2) (EPH HOMOLOGY KINASE-2)
EPHA6 OR EHK2 OR EHK-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maisonpierre P.C., Barrezueta N.X., Yancopoulo 
"Ehk-1 and Ehk-2: two novel members of the Epi 
kinase family with distinctive structures and 
Oncogene 8:3277-3288(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-i- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
-i- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -I- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A
-I- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE -
PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-SPRAGUE-DAWLEY; TISSUE-BRAIN; MEDLINE; 94067777.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EPA6_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249
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DAITEMDEHNRPIHTYQVCNVMEPNQNNWLRTNWISRDAAQKIYVEMKFTLRDCNSIPWV
                                                                                                                            CQLSILLLLSCSVLDSFGELIP------QPSNEVNLLDSKTIQGELGWISYPSHGW
                                                                                     CEVREFLL----QFGFFLPLLTAWTGDCSHVSNQVVLLDTSTVMGELGWKTYPLNGW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF01404;
                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9; pkinase; 1.
4; EPH_lbd; 1.
Tyrosine-protein
                                                                                                                                                                                                                                                                                          Ä,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata; Craniata; Vertebrata;
                                                                                                                                                                                                  68.4%;
                                                                                                                                                                                                                                                                                            106235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein;
                                                                                                                                                                                                                                                                                          MW;
                                                                                                                                                                             39;
                                                                                                                                                                                                                                                                                     ATP (BY SIMILARITY).
BY SIMILARITY.
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
A47DC78EDB2DEF30 CRC64;
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                                                                                                                                                                                                  Score 1003;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPHRIN TYPE-A RECEPTOR 6. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                           ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kinase; ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    (BY SIMILARITY). (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yancopoulos G.D.;
of the Eph receptor-like tyrosine ctures and neuronal expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal.
                                                                                                                                                                                                  DB 1;
3.3e-81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .112)
                                                                                                                                                                                                                       Length
                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia;
                                                                                                                                                                                                                         948;
                                                                                                                                                                             18;
                                                                                                                                                                           Gaps
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RESULT 6

EPA6_MOUSE

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AC 07 SECOND
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CC -1 S
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                                                                                                                                  PRINTS; PRO0014; FNYYPEIII.

PRINTS; PRO0109; TYRKINASE.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS001186; EGE_2; UNKNOWN_1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.

PFAM; PF00041; fn3; 2.

PFAM; PF000516; SAM; 1.

PFAM; PF000516; SAM; 1.

PFAM; PF011404; EPH_1bd; 1.

PFAM; PF011404; EPH_1bd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
EPHRIN TYPE-A RECEPTOR 6 PRECURSOR (E 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPA6_MOUSE
Q62413;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U58332; AAB53836.1; HSSP; P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lee A.M., Navaratnam D., Ichimiya S., Greene M.I., Davis J.G.;
"Cloning of m-ehk2 from the murine inner ear, an eph family ret
tyrosine kinase expressed in the developing and adult cochlea.

DNA Cell Biol. 15:817-825(1996).

DNA CELL BIOL. 15:817-825(1996).

FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BIN
EPHRIN-A1, -23, -33, -44 AND -45.

-1- CATALTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 97047913.
Lee A.M., Navaratr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KINASE RECEPTOR EHK-2) (EPH HOMOLOGY KINASE-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EPHA6 OR EHK2 OR EHK-2.
        TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
SIMILARTY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATI
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGI:108034; EPHA6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSSEERDTPKLYCGADGDWLVPLGRCICTTGYEE
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1 22 POTENTIAL.

23 1035 EPHRIN TYPE-A RECEPTOR 6.
23 549 EXTRACELLULAR (POTENTIAL).
550 570 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1035
                                                                                                                                        ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270
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                                                                                                                                        Phosphorylation,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BINDS
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Best I
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                                                                                                                                                                                                                                                                                                                  Q07496; Q90772;

Q1-NOV-1997 (Rel. 35, Cr

Q1-NOV-1997 (Rel. 35, La

Q1-NOV-1997 (Rel. 35, La

EPHRIN TYPE-A RECEPTOR 4

KINASE RECEPTOR CEK8).
Oncogene 8:1807-1813(1993).

- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY.
- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY.
- FUNCTION FOR FOR FOR MEMBERS OF THE EPHRIN-A FAMILY.
- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
- PROTEIN TYROSINE PHOSPHATE.
- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAIN
- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
NP_BIND
BINDING
ACT_SITE
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                         expressed
                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                             Gallus gallus (Chicken).
                                                                                                                Sajjadi F.G.,
                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                        Ando M.,
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
TISSUE-SPINAL CORL
                                                                                                                                                                                                                                                                                                           EPHA4 OR CEK8.
                                                                                                                             MEDLINE;
                                                                                                                                       TISSUE-EMBRYO
                                                                                                                                                                                                                             MEDLINE;
                                                                                                     "Five novel avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177
                                                                                                                                                                                                                                                                                                                                                                                                                                              237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 CQLSILLLLSCSVLDSFGELIP------QPSNEVNLLDSKTIQGELGWISYPSHGW 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match
                                                                                                                                                                                  receptor tyrosine kinase, ypes of motoneurons in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CEVREFLL-----QFGFFLPLLTAWTGDCSHVSNQVVLLDTTTVMGELGWKTYPLNGW 56
                                                                                                                                                                                                                                                                                                                                                                                      CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                             KSAEERDTPKLYCGADGDWLVPLGRCICSTGYEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCV 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGTCKETFNLYIMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DAITEMDEHNRPIHTYQVCNVMEPNQNNWLRTNWISRDAAQKIYVEMKFTLRDCNSIPWV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIERKGFYLAFQDIGACIALVSVRVFYKKCPFTVRSLAMFPDTIPRVDSSSLVEVRGSCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LGTCKETFNLYYIESDESHGTKFKPSQYIKIDTIAADESFTQMDLGDRILKLNTEIREVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                     Tanaka H.;
                                                                                                                                                                                                                            96404128.
                                                                                                                          93288394.
                                                                                                                                                 OF 138-986
                                                                                                                                                                                                                  Nakamura
                                                                                                                                                                       54:59-69(1996).
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630
636
797
797
342
396
                                                                                                               Fasquale
                                                                                                                                                                                                                                        CORD;
                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ā
                                                                                                    quale E.B.;
Eph-related
                                                                                                                                                                                                                M., Hirokawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1035
943
644
662
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409
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Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                PRECURSOR
                                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1002; DB 1;
Pred. No. 4.6e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                     tyrosine kinases
                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                ×;
                                                                                                                                                                                            Cek8,
                                                                                                                                                                                 spinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              560B264194A5EF74
                                                                                                                                                                                                                                                                                                                               ion update)
  (EC 2.7.1.112) (TYROSINE-PROTEIN
                                                                                                                                                                                                                 Tanaka
                                                                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                     986
                                                                                                                                                                                  cord
                                                                                                                                                                                            transiently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265
                                                                                                                                                                                                                                                                                                                                                                                                                                              270
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                                                                                                                                                                               during
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                                                                                                                                                                                                                Iwama
                                                                                                     are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1035;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                     differentially
                                                                                                                                                                                                                                                                        ; Archosauria; Gallus.
                                                                                                                                                                                            expressed
                                                                                                                                                                                                                Α.,
                                                                                                                                                                                                                Suda
   CATALYTIC
                                                         BINDS
AND A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                       A-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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Query Match
Best Local S
Matches 179
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PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.
PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROSITE; PS01186; EGF_2; UNKNOWN_1.
PROM; PF00041; fn3; 2.
PFAM; PF000536; SAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commentaties requires a license agreement (See http://www.isb-sib.ch/anror send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                            NP_BIND
BINDING
ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D38174; BAA07373.1; -. EMBL; Z19059; CAA79509.1; -. HSSP; P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase; Tyrosine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0014; FNTYPEIII.
PRINTS; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
 267
                         264
                                                   207
                                                                            205
                                                                                                       147
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                                                                                                                                                          87
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                                                                                                                                                                                                            27
                                                                                                                                                                                                                                     26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                  NWVPRNSAQKIYVELKETLRDCNSIPLVLGTCKETFNLYYMESDDDHGVKFREHQFTKID
                                                                                                                                                                                                                       PSNEVNLLDSKTIQGELGWISYP-SHGWEEISGVDEHYTDIRTYQVCNVWDHSQNNWLRT
                                                                                                                                                                                                           PANEVTLLDSRSVQGELGWIASPLEGGWEEVSIMDEKNTPIRTYQVCNVMEPSQNNWLRT
                         EERGFMCQ 271
                                                  TVRNLAQFPDTITGADTSSLVEVRGSCVNNSEEKDVPKMYCGADGEWLVPIGNCLCNAGY
                                                                            TVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGY
                                                                                                                                                       DWIPREGAQRVYIEIKFTLRDCNSLPGVMGTCKETFNLYYYESNNDKERFIRESQFAKID
EERNGECQ 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF01404;
                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                               ă,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EPH_lbd; 1.
                                                                                                                                                                                                                                                                                                                                          68.1%;
72.2%;
                                                                                                                                                                                                                                                                                                                               109482 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein;
POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (POTENTIAL).
POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                               35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPHRIN TYPE-A RECEPTOR 4.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III (BY SIN
FIBRONECTIN TYPE-III (BY SIN
PROTEIN KINASE.
                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                          S S
                                                                                                                                                                                                                                                                           Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kinase; ATP-binding; Phosphorylation
                                                                                                                                                                                                                                                            core 998; DB red. No. 9.7e Mismatches
                                                                                                                                                                                                                                                                                                                            -> G (IN REF. 2).
-> T (IN REF. 2).
BD88C2A5BD840A0F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal.
                                                                                                                                                                                                                                                                        DB 1;
.7e-81;
                                                                                                                                                                                                                                                           32;
                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL outstation
                                                                                                                                                                                                                                                            2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        collaboration -
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in no way
                                                                                                                                                                                                                                   84
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EPA4_HUMAN

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RR FOX 61

RR FOX 61

RR FOX 61

RR FOX 62

RR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO0014; FNTYPEIII.

PRINTS; PRO0109; TYRKINASE.ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00041; fn3; 2.

PFAM; PF00041; fn3; 2.

PFAM; PF000516; SAM; 1.

PFAM; PF005106; SAM; 1.

PFAM; PF01404; EPH_1bd; 1.

Transferase; Tyrosine-protein kinase; ATP-

Transferase; Tyrosine-protein kinase; ATP-
                              DOMAIN
DOMAIN
NP_BIND
BINDING
BINDING
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IF FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY.

EPHRIN-A1, -A4 AND -A5. BINDS MORE POORLY TO EPHRIN-A2

ICATALYTIC ACTUVITY: ATP + A PROTEIN TYROSINE - ADP +

PROTEIN TYROSINE PHOSPHATE.

ISUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAIN.

SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CADOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112
KINASE RECEPTOR SEK) (RECEPTOR PROTEIN-TYROSINE
EPHA4 OR SEK OR HEK8.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein-tyrosine kinases.
Oncogene 10:897-905(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=BRAIN;
MEDLINE; 95206782
Fox G.M., Holst P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L36645;
HSSP; P00523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPA4_HUMAN
                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA cloning and tissue distribution of five protein-tyrosine kinases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R., Welcher A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         602188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Holst P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAA74246.1; -.
2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
        109859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chute H.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein;
                                                 PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (POTENTIAL).
POTENTIAL.
POTENTIAL.
POTENTIAL.
     ¥
                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III (BY FIBRONECTIN TYPE-III (BY
     POTENTIAL.

1; 0C39C1152EDDD46F CRC64;
                                                                                                                                                                                                                                                                                                                                                  POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                          EPHRIN TYPE-A RECEPTOR 4. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lindberg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-binding; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.A., Janssen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      112)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2) (TYROSINE-PROTEIN KINASE HEK8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EPHRIN-A2 AND
- ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPH-like receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAINS.
THE CATALYTIC
                                                                                                                                                                                                                                                                       SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   collaboration
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Best Local :
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   PRINTS; P
PROSITE;
PROSITE;
PROSITE;
                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK-1) (EPH HOMOLOGY KINASE-1) (BRAIN-SPECIFIC KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOUSE
                                                             EMBL; U07357; AAA17038.1;
HSSP; P00523; 2PTK.
MGD; MGI:99654; EPHA5.
                                                                                                                                                                                                                                                                                                             Zhou R., Copeland T.D., Kromer L.F., Schulz N.T.; "Isolation and characterization of Bsk, a growth fac tyrosine kinase associated with the limbic system."; J. Neurosci. Res. 37:129-143(1994).
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN-BALB/C; TIS MEDLINE; 94194581.
                                                                                                                                                                                                                                                                                                                                                                                                                EPHAb OK BING. MOUSE).
MUS musculus (Mouse).
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                           EPHA5 OR EHK1 OR CEK7 OR
                                                                                                                                                                                                                              <del>-</del>
                                                                                                                                                                                                                                                      -
                                                                                                                                                                                                                                                                                                                                                            MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                         Eutheria; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                 EPHRIN-A1, -A2, -A3, -A4 AND -A5.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: BRAIN.

SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CAT.

DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.

SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                 FUNCTION: RECEPTOR FOR MEMBERS
        MGI-99654; EPHA5
TS; PRO0014; ENTYPEIII.
TS; PRO0109; TYRKINASE.
TITE; PS00107; PROTEIN_KINASE_TYR;
TITE; PS00109; PROTEIN_KINASE_TYR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLSC--SVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYP-SHGWEEISGVDEHYTPIR 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TEGEWLVPIGKCSCNAGYEERGFMCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYQVCNVMEPSQNNWLRTDWITREGAQRYYIEIKFTLRDCNSLPGVMGTCKETFNLYYYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADGEWLYPIGNCLCNAGHEERSGECQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDNDKERFIRENQFVKIDTIAADESFTQVDIGDRIMKLNTEIRDVGPLSKKGFYLAFQDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LFSCLFGICDAVTGSRVYPANEVTLLDSRSVQGELGWIASPLEGGWEEVSIMDEKNTPIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                        TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 995; Db 1,
                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata;
thi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                 OF THE EPHRIN-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         877
                                                                                                                    (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
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                                                                                                                                                                                                                                                                                                 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia;
                                                                                                                                                                                                                             THE CATALYTIC
                                                                                                                                                       restrictions
                                                                                                                                 and
                                                                                                                                                                                                                                                                                                                                   receptor-like
                                                                                                                                                                 gh a collaboration EMBL outstation -
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for
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in no way
commercial
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EPA5_RA
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Best Local Similarity
Matches 174; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE: PS00790; RECEPTOR_1
PROSITE: PS00791; RECEPTOR_1
PROSITE: PS01186; EGF_2; UNP
PFAM; PF00041; fn3; 1.
PFAM; PF00059; Pkinase; 1.
PFAM; PF000546; SAM; 1.
PFAM; PF01404; EPH_1bd; 1.
                                                                                                                                                         PERAS_RAT STANDARD: PRT; 1005 AA. PS4757; 01-OCT-1996 (Rel. 34, Created) 01-OCT-1996 (Rel. 34, Last sequence update) 01-NOV-1997 (Rel. 35, Last annotation update) PEHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2 7.112) KINASE RECEPTOR EHK-1) (EPH HOMOLOGY KINASE-1). EPHAS OR EKH1 OR EHK-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DOMAIN
NP_BIND
BINDING
ACT_SITE
CARBOHYD
CARBOHYD
SEQUENCE
                        Oncogene
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor;
SIGNAL
                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSMEM DOMAIN
STRAIN-SPRAGUE-DAWLEY;
                             Maisonpierre P.C., Barrezueta N.X., Yancopoulos G.D.; "Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine kinase family with distinctive structures and neuronal expression."; oncogene 8:3277-3288(1993).
                                                                                                                                                                                                                                                              RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
           SEQUENCE FROM
                                                                                           STRAIN-SPRAGUE-DAWLEY;
                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase;
                                                                                  MEDLINE;
                                                                                                                                                                                                                                                                                                                                  249
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                                                                                                                                                                                                                                                                                                                                                       VALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPPRMYCSTEG
                                                                                                                                                                                                                                                                                                                                                                                                                   DHGVKEREHQETKIDTIAADESETQMDLGDRILKLNTEIREVGPVNKKGEYLAFQDVGAC 189
                                                                                                                                                                                                                                                                                                           EWLVPIGKCMCKAGYEEKNGTCQ
                                                                                                                                                                                                                                                                                                                                EWLVPIGKCSCNAGYEERGFMCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                     VCKVMEQNQNNWLLTSWISNEGASRIFIELKFTLRDCNSLPGGLGTCKETFNMYYFESDD
                                                                            94067777.
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27
413
434
305
514
514
539
266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tyrosine-protein kinase; ATP-binding; Phosphorylation;
            N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RECEPTOR_TYR_KIN_V_1;
RECEPTOR_TYR_KIN_V_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26
877
412
433
877
399
775
528
546
639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.5%;
TISSUE=BRAIN
                                                                                            TISSUE-BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Glycoprotein;
BY SIMILA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 990; DB Pred. No. 4.3e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL).
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                           305
                                                                                                                                                                                                                                                                                                                                  271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPHRIN TYPE-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            990; DB 1;
No. 4.3e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Si
                                                                                                                                       Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ignal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RECEPTOR 5. (POTENTIAL).
                                                                                                                              Murinae;
```

(TYROSINE-PROTEIN

Mammalia; Rattus.

Length

Indels

Gaps

2

162

248 222

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EMBL; X78689; CAA55357.1; -.

HSSP; P00523; 2PTK.

PRINTS; PR00014; ENTYPEIII.

PRINTS; PR00109; TYRKINASE.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.

PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.
         CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                          CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                         NP_BIND
                                                                                                                                                                                                                                                                                                                                             TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                               ACT_SITE CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <del>:</del> :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Expression and developmental regulation of Ehk-1, a neuronal Elk-like receptor tyrosine kinase in brain.";
Neuroscience 63:163-178(1994).
                                                                                                 VARSPLIC
                                                                                                                                                    VARSPLIC
                                                                                                                                                                                                                  CARBOHYD
                                                                                                                                                                                                                            CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PFAM; PF00041; fn3;
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                                                                                                                                                                                                                                                                    CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ÷
                                                                                                                                                                                                                                                                                                                                                                                                            Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lassmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS TO EPHRIN-A1, -A2, -A3, -A4 AND -A5.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSED IN THE NERVOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYSTEM. PREDOMINANTLY EXPRESSED IN NEURONS.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00069; pkinase; PF01404; EPH_lbd;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95206467.
., Pfarr S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                H., Steck A.J.
                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane;
          170
566
578
669
708
979
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597
677
683
709
802
266
301
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                                                                                                                                                   358
                                                                                                                                                                                                                                                                                                                                                                                                      Tyrosine-protein kinase; ATP-binding; Phosphorylation; ansmembrane; Glycoprotein; Signal; Alternative splicing
                                                                                                                                                                                                   1005
575
596
1005
938
691
709
802
266
270
270
266
438
438
          170
566
578
708
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SPLICED FORMS).

SGSCCECGGGRASSLCAVAHPSLIW -
SPLICED FORMS).
D -> E (IN REF. 2).
G -> A (IN REF. 2).
G -> A (IN REF. 2).
G -> A (IN REF. 2).
T -> I (IN REF. 2).
T -> I (IN REF. 2).
                                                                                                                                                                                                                                                                                        PROTEIN KINASE.
ATP (BY SIMILAR
ATP (BY SIMILAR
BY SIMILARITY.
                                                                                                                   SPLICED FORMS;
VCRPGFFKASPHSQTCSKCPPHSYTHEEASTSCYCEKDYFR
RESDPFMACTR -> G (IN SPLICED FORMS),
RPPSAPRNAISNVNETSVFLEWIPPADTGGGKDVSYYILCK
KCNSHAGYCEECGGHYRYLPQQIGLKNTSVMMADPLAHTNY
TEPTEAVMGYSDLSPGTRQYYSYNYTINQAA -> T (IN
                                                                                                                                                                                                                           POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                POTENTIAL.
GRRRTQGRGGG -> DADGPRAQASWCHARR
                                                                                                                                                                                        SPLICED FORMS).
                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                  EPHRIN TYPE-A RECEPTOR 5
                                                                                                                                                                                                                                                                               POTENTIAL.
                                                                                                                                                                                                                                                                                                      (BY SIMILARITY).
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Best Local S
Matches 173
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D1-OCT-1996 (Rel. 34, Created)

O1-OCT-1996 (Rel. 34, Last sequence update)

15-JUL-1998 (Rel. 36, Last annotation update)

EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN-KINASE RECEPTOR EHK-1) (EPH HOMOLOGY KINASE-1) (RECEPTOR PROTEIN-TYROSINE KINASE HEK7).
                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bioinformatics Institute There are a constituted to the European Bio
                                                                                                                                                                                                                                                                                                                                                                                           "cDNA cloning and tissue distribution protein-tyrosine kinases."; Oncogene 10:897-905(1995).
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Eukaryota; Metazoa; Chordata; C:
Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Fox G.M., Holst P
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Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Basu R., Welcher A.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 25-1037 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISSUE-BRAIN,
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                                                                                                         SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATADOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                    SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: ALMOST EXCLUSIVELY EXPRESSE
                                                                                                                                                                                                                                                                                                  FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A1, -A2, -A3, -A4 AND -A5.
CATALYTIC ACTIVITY: ATP + A PROTEIN PROTEIN TYROSINE PHOSPHATE.
                                                                                                                                                              SYSTEM.
SIMILARITY: TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HUMAN
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institutions as long
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Pred.
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                There are
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as its content
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is not removed agreement (See

noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/

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RESULT 12
EPA4_MOUSE
ID EPA4_M
AC Q03137
DT 01-OCT
DT 01-OCT
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 173
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PRINTS; PRO0109; TYRKINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS01186; EGF_2; UNKNOWN_1.
EPA4_MOUSE
Q03137;
Q1-OCT-1994
Q1-OCT-1994
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HSSP; P00523;
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                                                                                         281
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1; PF00069; pkinase; 1
1; PF00536; SAM; 1.
1; PF01404; EPH_lbd; 1
                                                                                      EWLVPIGKCMCKAGYEEKNGTCQ
                                                                                                     EWLVPIGKCSCNAGYEERGFMCQ
                                                                                                                                QNGRNIKENQYIKIDTIAADESFTELDLGDRVMKLNTEVRDVGPLSKKGFYLAFQDVGAC
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                                                                                                                                                                                                                                   VCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDD
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                                                                                                                                                                                                                                                                  LLLCAALRT - - - LLASPSNEVNLLDSRTVMGDLGWIAFPKNGWEEIGEVDENYAPIHTYQ
                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane;
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 (Rel.
                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                               Tyrosine-protein
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; AAA74245.1; -.
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                                 STANDARD;
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573
593
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4436
619
30, Created)
30, Last sequence update)
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65.8%;
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POTENTIAL
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ATP (BY SIMILARITY).
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Pred. No. 1.8e
44; Mismatches
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CYTOPLASMIC (PO
                                                                                                             271
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                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          kinase; ATP-binding; Phosphorylation;
pprotein; Signal; Alternative splicing
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(BY SIMILARITY).
(BY SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                     Length 1037;
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MGD; MGI:98277; EPHA4.

PRINTS; PRO0014; PNTYPEIII.

PRINTS; PRO0019; TYRKINASE_ATP; 1.

PROSITE; PS00107; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00709; RECEPTOR_TYR_KIN_V_1; 1.

PROSITE; PS00709; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS007091; RECEPTOR_TYR_KIN_V_2; 1.

PROSITE; PS007091; RECEPTOR_TYR_KIN_V_2; 1.

PFAM; PF00041; fn3; 2.

PFAM; PF000540; SAM; 1.

PFAM; PF00536; SAM; 1.

PFAM; PF01404; EPH_1bd; 1.
Receptor;
SIGNAL
SIGNAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EPHA4 OR SEK.

Mus musculus (Mouse).

Eukaryota; Metazoa; C

Eutheria; Rodentia; S
                                                                                                                                                                                                                                                   EMBL; X65138;
EMBL; X57241;
EMBL; S57168;
HSSP; P00523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GHardi-Hebenstreit P., Ni
Chestier A., Wilkinson D.G
Oncogene 8:1103-1103(1993)
                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "An Eph-related receptor protein texpressed in the developing mouse Oncogene 7:2499-2506(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Last annotation EPHRIN TYPE-A RECEPTOR 4 PRECURSOR (ECKINASE RECEPTOR SEK) (MPK-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gilardi-Hebenstreit P., N
Chestier A., Wilkinson D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL; TIS: MEDLINE; 93096484
                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ERRATUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no was
                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY.
EPHRIN-A1, -A4 AND -A5. BINDS MORE POORLY TO EPHRIN-A2
MAY PLAY A ROLE IN A SIGNAL TRANSDUCTION PROCESS INVOLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93205393
                                                                                          Transmembrane;
   548
570
325
436
                                                                                                                                                                                                                                                  ; CAA46268.1; -.; CAA40517.1; -.; AAB25836.1; -.; 2PTK.
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TISSUE=EMBRYONIC
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986
547
569
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532
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Chordata; Craniata; Vei
Sciurognathi; Muridae;
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.G., Charnay P.;
protein tyrosine kinase
ing mouse hindbrain.";
                                                                                         otein kinase;
Glycoprotein;
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                                           EPHRIN TYPE-A
EXTRACELLULAR
POTENTIAL.
        CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III (BY SIMILARITY).
FIBRONECTIN TYPE-III (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Charnay
                                                                             POTENTIAL
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Charnay P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BRAIN;
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                                                                                   ATP-binding; Phospnon: Signal; Alternative
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C 2.7.1.112)
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ae; Murinae;
                                                      RECEPTOR 4. (POTENTIAL).
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                                                                                      Phosphorylation; ernative splicing
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THE CATALYTIC
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EXPRESSED
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Best Local S
Matches 177
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BINDING
ACT_SITE
MOD_RES
CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OVT-1997 (Rel. 35, Last annotation updat
EPHRIN TYPE-A RECEPTOR 5 PRECURSOR (EC 2.7.
KINASE RECEPTOR CEK7).
                                                                                                                                                                                                                                                                                                                                                                                                   EPA5_CHICK P54755;
                                                                                                                                                                         MEDLINE; 95047429.

Slever D.A., Verderame M.F.;

"Identification of a complete Cek7 receptor protein tyrosine kina:

"Identification of a complete Cek7 receptor protein tyrosine kina:

coding sequence and cDNAs of alternatively spliced transcripts.";

Gene 148:219-226(1994).

-I- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS '
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                                                                                                                                                                                                                                                                                      EPHA5 OR CEK7.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata;
Neognathae; Galliformes; Phas;
                                                                                                                                                                                                                                                                                                                                                                                                                             CHICK
                                                                                                                                                                                                                                                      TISSUE-BODY WALL;
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                           EPHRIN-A1, -A2, -A3, -A4 AND -A5.

CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

ALTERNATIVE PRODUCTS: A NUMBER OF VARIANTS ARE PRODUCED BY ALTERNATIVE SPLICING.

ALTERNATIVE SPLICING.

SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATAL DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.

SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPF
||||||||:::||||::||||
TIAADESFTQVDIGDRIMKLNTEIRDVGPLSKKGFYLAFQDVGACIALVSVRVFYKKCPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDDDHGVKFREHQFTKID
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653
746
779
235
408
423
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71
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                                                                                                                                                                                                                                                                                      data; Craniata; Vertebrata;
Phasianidae; Phasianinae; (
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ATP (BY SIMILARITY).
BY SIMILARITY).
BY SIMILARITY.
PHOSPHORYLATION (AUTO-) (POTENTIAL).
POTENTIAL.
POTENTIAL.
POTENTIAL.
POTENTIAL.
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Pred. No. 3.86
35; Mismatches
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V; D16AD8B85668C80E CRC64;
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2.7.1.112)
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                                                                                       CATALYTIC
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DR PROSITE; PS00104; FNTYPEIII.

DR PRINTS; PR00014; FNTYPEIII.

DR PROSITE; PS00107; PROTEIN_KINASE_TYP; 1.

DR PROSITE; PS00119; PROTEIN_KINASE_TYR; 1.

DR PROSITE; PS00119; PROTEIN_KINASE_DOM; 1.

DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

DR PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

DR PFAM; PF00041; fn3; 2.

DR PFAM; PF00069; pkinase; 1.

DR PFAM; PF000536; SAM; 1.

DR PFAM; PF001404; EPH_1bd; 1.

KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;

KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
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Matches 170
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EMBL; U03910;
EMBL; U03910;
HSSP; P00523;
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DOMAIN
TRANSMEM
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CARBOHYD
VARSPLIC
VARSPLIC
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CARBOHYD
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DOMAIN
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BINDING
ACT_SITE
CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                     SEQUENCE
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257
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                                                                                                           LLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDEHYTPIRTYQ
EWLVPIGKCLCKAGYEEKNNTCQ
         EWLVPIGKCSCNAGYEERGEMCQ
                                              VALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPPRMYCSTEG
                                     TALVSVRVYYKKCPSVIRNLARFPDTITGADSSQLLEVSGVCVNHSVTDEAPKMHCSAEG
                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                    1013
                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                    ΑΑ;
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112245 MW;
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SCIDHGGGMASSIRAVAXPSLIW
1 AND ISOFORM 2).
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Pred. No. 3.4e
37; Mismatches
                 271
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PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
279
                                                                                                                                                                                                                                                                                                                                                                             EPHRIN TYPE-A RECEPTOR 5. EXTRACELLULAR (POTENTIAL). POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                 BY SIMILARITY.
                                                                                                                                                                                                                                    AC36FD6AEBF38382 CRC64;
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3.4e-76;
nes 52;
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RESULT 14
EPA7_HUMAN
ID EPA7_HUMAN
AC Q15375;
DT 01-NOV-1997

STANDARD;

PRT;

998

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(Rel. 35, Created)

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R PRINTS; PRO0109; TYRKINASE.

R PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

2 PROSITE; PS00710; PROTEIN_KINASE_DOM; 1.

2 PROSITE; PS00790; RECEPTOR_TYR_KIN_V_1; 1.

3 PROSITE; PS00791; RECEPTOR_TYR_KIN_V_2; 1.

4 PROSITE; PS001186; EGF_2; UNKNOWN_1.
              Query Match
Best Local
     Matches
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15-JUL-1998 (Rel. 36, Last and
EPHRIN TYPE-A RECEPTOR 7 PRECI
KIMASE RECEPTOR EHR-3) (EPH HO
TYROSINE KIMASE HEK11).
                                                                                                   NP_BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -I- FUNCTION: RECEPTOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BI EPHRIN-AI, "A2," A3, "A4 AND "A5.
-I- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE PHOSPHATE.
-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-I- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATA-DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
-I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                            PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L36642; AAA74243.1; -. HSSP; P00523; 2PTK.
MIM; 602190; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein-tyrosine kinases.";
Oncogene 10:897-905(1995).
                                                                                                                                                                                                                                                                                PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PODIA Cloning and tissue distribution of five human "CDNA Cloning and tissue distribution of five human"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                      DOMAIN
                                                                                                                                                                   DOMAIN
                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                    Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PROCO14
PRINTS; PROCO109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-BRAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                         CARBOHYD
                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                      Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                             PF00041; fn3; 2.
PF00069; pkinase; 1.
PF00536; SAM; 1.
PF01404; EPH_lbd; 1.
               Similarity
                                                                                                                                                                                                                                                       Transmembrane;
                                                                                       Tyrosine-protein
                                                                                                                                                                                                                                                                                                                                                                                                                     FNTYPEIII.
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6647
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758
758
                                                                112096
             68.4%;
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Last annotation update)
R 7 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN) (EPH HOMOLOGY KINASE-3) (RECEPTOR PROTEIN-
                                                                                                                                                                                                                                         Glycoprotein;
POTENTIAL.
                                                                W.
   39;
 Score 927.5; D
Pred. No. 1.8e-
9; Mismatches
                                                                                                                                                             POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
                                                                                                               ATP
ATP
BY S
                                                                           POTENTIAL
                                                                                      PHOSPHORYLATION (AUTO-)
POTENTIAL.
                                                                                                                                                                                                              EPHRIN TYPE-A RECEPTOR 7. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                               kinase; ATP-binding;
                                                                                                               SIMILARITY
                                                                                                                        TEIN KINASE.
(BY SIMILARITY).
(BY SIMILARITY).
                                                              479B9CA0D2BB06EB
                                                                                                                                                                                                                                                    Signal.
                        DB 1;
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A Copeland N.G., Tempest H.V., Warren S., Muir E., Schilling H.,
A Copeland N.G., Tempest H.V., Warren S., Muir E., Schilling H.,
A Copeland N.G., Tempest H.V., Warren S., Muir E., Schilling H.,
A Copeland N.G., Tempest H.V., Warren S., Muir E., Schilling H.,
A Copeland N.G., Tempest H.V., Warren S., Muir E., Schilling H.,
Embryo brain kinase: a novel gene of the eph/elk receptor tyros
T kinase family.",
Mech. Dev. 52:319-341(1995).
C Hency S., Schilling H.V., MEMBERS OF THE EPHRIN-A FAMILY. BINDS
C HINGLING FOR FOR MEMBERS OF THE EPHRIN-A FAMILY. BINDS
C HERINATIVE ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.
C HORL-Z, MDRI-TI AND MDRI-T2) ARE PRODUCED BY ALTERNATIVE
C HALTERNATIVE PRODUCTS: FIVE FORMS OF THE PROTEIN (MDRI-MDRI-T2), MDRI-T1 AND MDRI-T2) ARE PRODUCED BY ALTERNATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _MOUSE STANDARD; PRT; 998 AA.

Q61772; Q61773; Q61774; Q61505;

Q1-NOV-1997 (Rel. 35, Created)

Q1-NOV-1997 (Rel. 35, Last sequence update)

Q1-NOV-1997 (Rel. 35, Last annotation update)

EPHRIN TYPE-A RECEPTOR 7 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR EHK-3) (EPH HOMOLOGY KINASE-3) (EMBRYONIC BRAIN KINASE) (EBK) (DEVELOPMENTAL KINASE 1) (MDK-1).

EPHA7 OR EHK3 OR EBK OR MDK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MDK1, a novel receptor ty nervous system."; Oncogene 10:97-108(1995).
                                                 This
                                  between
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"Identification of alternatively spl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.,
STRAIN-BALB/C; TISS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata;
Eutheria; Rodentia; Sciurognathi; Murid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; C
                                                                                                                                                                                                                                                                                                                                                                                                                                     FISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                 MDK1.
TISSUE SPECIFICITY: WIDELY EXPRESSED IN EMBRYO. IN ADULT,
EXPRESSION RESTRICTED TO HIPPOCAMPUS, TESTIS AND SPLEEN.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CAT!
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
DOMAIN. BELONGS TO THE EPHRIN RECEPTOR FAMILY.
ween the Swiss Institute of Bloinfi
European Bioinformatics Institute.
by non-profit institute.
                                                                                                                                                                                   SPLICING
                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPF
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R HSSP; P00523; ZFIA.

JR MGD; MGI:95276; EPHA7.

JR PRINTS; PR00014; FITYPEIII.

DR PRINTS; PR00109; TYRKINASE_TYP; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_TYP; 1.

DR PROSITE; PS00109; PROTEIN_KINASE_TYP; 1.

DR PROSITE; PS00019; RECEPTOR_TYR_KIN_V_1; 1.

DR PROSITE; PS00790; RECEPTOR_TYR_KIN_V_2; 1.

DR PROSITE; PS001186; RECEPTOR_TYR_KIN_V_2; 1.

DR PROSITE; PS001186; REGE_2; UNKNOWN_1.

DR PRAM; PF00041; fn3; 2.

DR PRAM; PF000536; SAM; 1.

DR PRAM; PF00536; SAM; 1.

DR PRAM; PF01404; EPH_lbd; 1.
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PHOSPHOKYLATION (AUTO-) (BY SIMILARITY).

POTENTIAL.

POTENTIAL.

POTENTIAL.

MISSING (IN ISOFORM MDK1-2).

MISSING (IN ISOFORM MDK1-2).

MISSING (IN ISOFORM MDK1-2).

FKFPGTKYID -> SLVTNEHLSYL (IN ISOFORM MTK1-T1).

MISSING (IN ISOFORM MDK1-T1).

FKFPGTKYIDPETYEDPURAVHOPAK -> SLYRERGDGM EXTOHNKKWMIASCSRL (IN ISOFORM MDK1-T2).

MISSING (IN ISOFORM MDK1-T2).
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
FIBRONECTIN TYPE-III.
PROTEIN KINASE.
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Pred. No. 2.2e
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Result

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45	4.4	43	42	41	40	39	38	37	36	35	34	33	32	31
86	87.5	88	89.5	93.5	96	250.5	397.5	493	510	510	528.5	569.5	589	594.5
5. 9	6.0	6.0	6.1	6.4	6.5	17.1	27.1	33.6	34.8	34.8	36.1	38.8	40.2	40.6
919	788	1376	668	982	698	1122	1019	987	987	987	1006	849	938	952
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T29581	I51530	VGIHJ2	T05803	S58881	H71401	T42400	T13039	A54092	I48652	I48953	JC5526	I50617	I49071	150612
hypothetical prote	integrin beta-3 su	٠.	hypothetical prote	muts protein homol	probable A6 anther	Eph receptor tyros	tyrosine kinase re	protein-tyrosine k	mouse developmenta	eph-related recept	kinase-defective E	protein-tyrosine k	protein kinase – m	protein-tyrosine k

ALIGNMENTS

Minimum Maximum

Searched:

Sequence:

Run

A; Molecule: type: protein
A; Molecule: type: protein
A; Molecules: 21-39,810-860 <MIZ>
C; Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repea
C; Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferas
F;1-20/Domain: signal sequence *status predicted <SIG>
F;21-983/Product: protein-tyrosine kinase hek #status experimental <MAT>
F;42-565/Domain: transmembrane *status predicted <TMM>
F;619-885/Domain: protein kinase homology <KIN>
F;627-635/Region: protein kinase ATP-binding motif
F;232,337,391,404,493/Binding site: carbohydrate (Asn) (covalent) *status predicted protein tyrosine kinase (EC 2.7.1.112) hek precursor - human (Species: Homo sapiens (man) (man) (Species: Homo sapiens (man) (Part: 31-Dec-1993 #text_change 18-Jun-1999 (C.Accession: A38224, B38224 (Part: A3224) (Part: A3224 (Part: A3224) (Part: A3224 (Part: A3224) (Part: A3224 (Part: A3224) (Pa A; Molecule type: mRNA
A; Residues: 1-983 < MIC>
A; Cross-references: GB:N83941; NID:g183931; PIDN:AAA58633.1;
A; Experimental source: pre-B-cell leukemia cell line LK63
A; Note: sequence extracted from NCBI backbone (NCBIP:86627)
A; Accession: B38224 Query Match
Best Local Similarity
Matches 271; Conserv 241 RMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ 271 1 MDCQLSILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDE 60
1 MDCQLSILLLLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDE 60 HYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETF 120 LAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCVNNSKEEDPP RMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ NLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFY 180 LAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCVNNSKEEDPP 100.0%; ilarity 100.0%; Conservative 0; 0 Score 1466; DB 2; Pred. No. 2.9e-122; ; Mismatches 0; 271 Length Indels PID:g183932 0 Gaps 180 240 240 0;

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C; Species: Mus musculus (hou C; Date: 22-Apr-1993 #sequenc C; Accession: A45583 R; Sajjadi, F.G.; Pasquale, E New Biol. 3, 769-778, 1991 A; Title: Identification of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Identification of a new eph-related receptor tyrosine kinase gene f A;Reference number: A45583; MUID:92031278
A;Accession: A45583
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-983 <SAJ>
A;Cross references: GB:M68513; NID:g199119; PIDN:AAA39521.1; PID:g199120
A;Cross references: GB:M68513; NID:g199119; PIDN:AAA39521.1; PID:g199120
A;Note: sequence extracted from NCBI backbone (NCBIN:62398, NCBIP:62401)
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type C;Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein F;G19-885/Domain: protein kinase homology <KIN>
F;G27-635/Region: protein kinase ATP-binding motif
                                                                             A; Molecule type: mRNA
A; Residues: 1-983 <SAJ>
A; Cross-references: GB.M68514; NID: 9454809; PIDN: AAA48666.1; PID: 9211447
A; Cross-references: GB.M68514; NID: 9454809; PIDN: AAA48666.1; PID: 9211447
A; Note: sequence extracted from NCBI backbone (NCBIN: 62405, NCBIP: 62411)
C; Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type
C; Keywords: ATP; autophosphorylation; phosphoprotein; transmembrane protein
F; 619-885/Domain: protein kinase homology <KINV
F; 627-635/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                  receptor tyrosine kinase Cek4 - chicken
C:Species: Gallus gallus (chicken)
C:Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 18-Jun-1999
C:Accession: B45583
R:Sajjadi, F.G.: Pasquale, E.B.: Subramani, S.
New Biol. 3, 769-778, 1991
A:Ritle: Identification of a new eph-related receptor tyrosine kinase gene :
A:Reference number: A45583; MUID:92031278
A:Accession: B45583
A:Status: preliminary
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-Apr-1993 #sequence_revision
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8; Mismatches
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C;Superfamily: protein tyrosine kinase, receptor
C;Keywords: ATP; transmembrane protein
F;628-936/Domain: protein kinase homology <KIN>
F;636-644/Region: protein kinase ATP-binding moti
 receptor protein-tyrosine kinase - C; Species: Homo sapiens (man) C; Date: 29-May-1998 #sequence_revi:
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A;Molecule type: mRNA
A;Residues: 1-948 <MAI>
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A;Title: Ehk-1 and Ehk-2: two novel members of the Eph re A;Reference number: S49015; MUID:94067777
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C;Accession: S51605
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C; Species: Rattus norvegicus (Norway rat)
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 #sequence_revision
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Pred. No. 4.1e-81;
9; Mismatches 37;
                                  human
 29-мау-1998
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#text_change
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PVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCV
                                                                                                                 LGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVG
                                                                                                                                                                                                            EEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLV
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PIERKGFYLAFQDIGACIALVSVRVFYKKCPFTVRNLAMFPDTIPRVDSSSLVEVRGSCV
                                                                                           LGTCKETFTLYYIESDESHGTKFKPSQYIKIDTIAADESFTQMDLGDRILKLNTEVREVG
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repea

18-Jun-1999

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C;Accession: I78844
R;Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Ja
Oncogene 10, 897-905, 1995
A;Title: cDNA cloning and tissue distribution of five hum
A;Reference number: I58351; MUID:95206782
A;Accession: I78844
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-986 <RES>
A;Cross-references: GB:L36645; NID:9551613; PIDN:AAA74246
C;Genetics:
A;Gene: HEK8
C;Superfamily: protein-tyrosine kinase, receptor type eph
F;619-885/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                    A:Gene: Bsk
C:Superfamily: I
C:Superfamily: I
C:Keywords: ATP:
F:512-778/Domain
F:520-528/Region
F:801-868/Domain
                                                                                                                                                                                                                                                                                                                brain-specific kinase - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C;Accession: 148967
R;Zhou, R.R.; Copeland, T.D.; Kromer, L.F.; Schulz, N.T.
J. Neurosci. Res. 37, 129-143, 1994
A;Title: Isolation and characterization of Bsk, a growth factor receptor-like A;Accession: 148967; MUID:94194581
A;Accession: 148967
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-877 <RES>
A;Cross-references: EMBL:U07357; NID:9466369; PIDN:AAA17038.1; PID:9466370
C;Genetics:
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                                                                                                                                                                                                                   Keywords: ATP; transmembrane protein;512-778/Domain: protein kinase homolo;520-528/Region: protein kinase ATP-b
                                                                                                   Query Match
Best Local Similarity
Matches 174; Conser
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                                                                                                                                                                                                    801-868/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPPRMYCS 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYME
                                          LLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDEHYTPIRTYQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADGEWLYPIGNCLCNAGHEERSGECQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TEGEWLVPIGKCSCNAGYEERGFMCQ 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYQVCNVMEPSQNNWLRTDWITREGAQRVYIEIKFTLRDCNSLPGVMGTCKETFNLYYYE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LFSCLFGICDAVTGSRVYPANEVTLLDSRSVQGELGWIASPLEGGWEEVSIMDEKNTPIR 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GACIALVSVRVFYKKCPLTVRNLAQFPDTITGADTSSLVEVRGSCVNNSEEKDVPKMYCG
                        LLLCAALRT - - - LLASPSNEVNLLDSRTVMGDLGWIAFPKNGWEEIGEVDENYAPIHTYQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183;
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protein kinase ATP-binding mo
SAM homology <SAM>
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                                                                                                                       67.5%;
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                                                                                                   Score 990; DE Pred. No. 5.36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 995; DB 2;
Pred. No. 2.2e-80;
7; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           274
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                                                                                                                                                                                                                     motif
                                                                                                                     DB 2;
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                                                                                                                                        Length 877
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Oncogene 8, 3277-328
A;Title: Ehk-1 and 1
A;Reference number:
                                  R:Maisonpierre, P.C.; Barrezueta, N.X.; Oncogene 8, 3277-3288, 1993
                                                                         receptor-like tyrosine kinase Ehk-1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change
C;Accession: S51603
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S51603
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A;Molecule type: mRNA
A;Residues: 1-898 <TAY>
A;Residues: 1-898 <TAY>
A;Cross-references: EMBL:X78689; NID:g531543; PIDN:CAA55357.1;
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibr C;Keywords: ATP; transmembrane protein
E;568-834/Domain: protein kinase homology <KIN>
F;576-584/Region: protein kinase ATP-binding motif
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A:Description: Expression and developmental regula
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor tyrosine kinase - rat

C; Species: Rattus norvegicus (Norway rat)
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999
C; Date: 13-Jun-1995 #text_change 18-Jun-1999
C; Date: 13-Jun-1995 #text_change 18-Jun-1995
C; Date: 13-Jun-1995
C; Date: 13-Jun-1
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Best Local Similarity
Matches 174; Conserv
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                                                                                                                                                                                                                                               VALVSVRYYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPPRMYCSTEG 248
                                                                                                                                                                                                                                                                                                                                                                                 VCKVMEQNQNNWLLTSWISNEGASRIFIELKFTLRDCNSLPGGLGTCKETFNMYYFESDD 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LLLCAALRT---LLASPSNEVNLLDSRTVLGDLGWIAFPKNGWEEIGEVDENYAPIHTYQ 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLSCSVLDSFGELIPQPSNEVNLLDSKTIQGELGWISYPSHGWEEISGVDEHYTPIRTYQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPPRMYCSTEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                             VCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDD 129
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EWLVPIGKCMCKAGYEEKNGTCQ
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repea

277-3288, 1993 1 and Ehk-2: tw 1 and Ekk-2; tw

two novel members 5; MUID:94067777

Eph

receptor-like

tyrosine

kinase

Yancopoulos, G. of the

28-May-1999

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receptor-like tyrosine kinase Ehk-1 - rat
receptor-like tyrosine kinase Ehk-1 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 29-May-1998
C;Accession: 551604
R;Maisonpierre, P.C.: Barrezueta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A;Title: Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine kinase fam
A;Reference number: S49015; MUID:94067777
A;Accession: S51604
A;Status: prediminary
A;Cossion: S51604
A;Status: prediminary
A;Coss-references: EMBL:S68029
A;Coss-references: EMBL:S68029
A;Note: the authors translated the codon GAC for residue 170 as Glu
C;Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat h
C;Keywords: ATP; transmembrane protein
C;Keywords: ATP; transmembrane protein
F;651-917/Domain: protein kinase homology <KIN>
F;659-667/Region: protein kinase ATP-binding motif
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A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-893 < MAIN
A; Cross-references: EMBL: S68028
A; Cross-references: EMBL: S68028
A; Cross-references: translated the codon GAC for residue 170 as Glu
C; Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin
C; Keywords: ATP; transmembrane protein
C; Keywords: ATP; transmembrane protein
F; 563-829/Domain: protein kinase ATP-binding motif
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Matches 173
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Best Local S
Matches 173
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                   DHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGAC
                                                      VCKVMEQNQNNWLLTSWISNEGASRIFIELKFTLRDCNSLPGGLGTCKETFNMYYFESDD
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73; Conservative
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67.2%;
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Pred. No. 1.7e-79;
5; Mismatches 41
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-305,'G',359-1005 <MA2>
A;Residues: 1-305,'G',359-1005 <MA2>
A;Cross references: EMBL:S68026
A;Cross references: EMBL:S68026
A;Note: the authors translated the codon GAC for rec;Superfamily: protein tyrosine kinase, receptor ty C;Keywords: ATP: transmembrane protein
F;675-941/Domain: protein kinase homology <KIN>
F;683-691/Region: protein kinase ATP-binding motif
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C;Date: 14-Jul-1995 *sequence_revision 21-Jul-1995 *text_change 28-May-1999
C;Accession: S49015; S51602
R;Maisonpierre, P.C.; Barrezueta, N.X.; Yancopoulos, G.D.
Oncogene 8, 3277-3288, 1993
A;Title: Bik-1 and Bik-2; two novel members of the Eph receptor-like tyrosine kinase
A;Reference number: S49015; MUID:94067777
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S49015
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A; Residues: 1-1005 <AAI>
A; Cross-references: EMBL:S68024
A; Note: the authors translated
A; Accession: $51602
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A; Accession: S49015
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Best Local
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                                                                    IALVSVRVYYKKCPSVVRHLAVFPDTITGADSSQLLEVSGSCVNHSVTDDPPKMHCSAEG
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65.88;
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Pred. No. 1.7e-79;
5; Mismatches 41
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receptor protein-tyrosine kinase - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 18-Jun-1999
C;Accession: I78843
R;Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu, Oncogene 10, 897-905, 1995
Oncogene 10, 897-905, 1995

Basu,

protein

11

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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-31,55-986 <GIL>
A; Cross-references: EMBL:X65138
C; Genetics:
A; Gene: Sek
C; Genetics:
A; Gene: Sek
C; Superfamily: protein-tyrosine kinase, receptor type eph; fibronectin type III repeat l
C; Keywords: ATP; autophosphorylation; glycoprotein; phosphoprotein; phosphotransferase;
F; 1-15/Domain: signal sequence #status predicted <SIG>
F; 16-986/Product: protein-tyrosine kinase Eph #status predicted <MAT>
F; 548-569/Domain: transmembrane #status predicted <TMM>
F; 519-885/Domain: protein kinase homology <KIN>
F; 619-885/Domain: protein kinase homology <KIN>
F; 908-974/Domain: SAM homology <SAM>
F; 235,340,408,423/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                     protein-tyrosine kinase (EC 2.7.1.112) Eph precursor - C;Species: Mus musculus (house mouse) C;Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #te; C;Accession: S78059; S30505; IS8366 R;Charnay, P.
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S78059
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F: 627-893/Domain:
F: 916-982/Domain:
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A; Residues: 1-991 < RES>
A; Cross-references: GB:L36644;
C; Genetics:
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A; Accession: 178843
A; Status: preliminary;
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Best Local S
Matches 173
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in: protein kinase homology
in: SAM homology <SAM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translated
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65.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 984; DB 2;
Pred. No. 2.1e-79;
4; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279
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                                                                                                                                                                                                                                                                                                                                                                                                         March 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              receptor
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Match

66

Score

980;

BB

2

Length 986;

RESULT

14

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                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: protein-tyrosine kinase, receptor type eph;
C;Keywords: ATP; transmembrane protein
F;618-884/Domain: protein kinase homology <KIN>
F;626-634/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Accession: I51549

R;Winning, R.S.; Sargent, T.D.

Mech. Dev. 46, 219-229, 1994

A;Title: Pagliaccio, a member of the Eph

A;Reference number: I51549; MUID:95001564

A;Accession: I51549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: Pag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-985 <WIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor tyrosine kinase - African clawed C; Species: Xenopus laevis (African clawed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                            Best Local Similarity Matches 175; Conserv
                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                               145
 267
                                264
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                                                                                                                         TIAADESFTQVDIGDRIMKLNTEVRDVGPLSKKGFYLAFQDVGACIALVSVRVFYKKCPL
                                                                                                                                          TIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPF 204
                                                                                                                                                                                                            NWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDDDHGVKFREHQFTKID 144
                                                              .TVRNLAQFPDTITGSDTSSLVEVRGSCVDNSEEKDVPKMYCGADGEWLVPIGNCLCNAGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIAADESFTQMDLGDRILKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPF 204
                              EERGFMCQ
                                                                            TVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGY 263
                                                                                                                                                                                                                                                                           PSNEVNLLDSKTIQGELGWISYP-SHGWEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRT 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGY 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDDDHGVKFREHQFTKID 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSNEVNLLDSKTIQGELGWISYP-SHGWEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRT
EEHNGGCQ
                                                                                                                                                                                          DWIPRSGAQRVYVEIKFTLRDCNSLPGVMGTCKETFNLYYYESNNDKERFIRETQYVKID 146
                                                                                                                                                                                                                                                          PASEVTLLDSRSVQGELGWIASPLEGGWEEVSIMDEKNTPIRTYQVCNVMESSQNNWLRT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEQNGECO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EERGFMCQ 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TVRNLAQFPDTITGADTSSLVEVRGSCVNNSEEKDVPKMYCGADGEWLVPIGNCLCNAGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIAADESFTQVDIGDRIMKLNTEIRDVGPLSKKGFYLAFQDVGACIALVSVRVFYKKCPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DWITREGAORVYIEIKFTLRDCNSLPGVMGTCKETFNLYYYESDNDKERFIRESOFGKTD 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PANEVTLLDSRSVQGELGWIASPLEGGWEEVSIMDEKNTPIRTYQVCNVMEASQNNWLRT 86
                                                                                                                                                                                                                                                                                                                            Conservative
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274
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70.6%;
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35; Mismatches
                                                                                                                                                                                                                                                                                                                          Score 977; DB 2;
Pred. No. 8.7e-79;
9; Mismatches 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-Sep-1996 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        family of receptor
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ches 34;
                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PID: g416403
                                                                                                                                                                                                                                                                                                                         2;
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repea

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A; Reference number: 158
A; Accession: 158351
A; Status: preliminary;
A; Molecule type: mRNA
A; Residues: 1-998 < RES>
A; Cross-references: GB:
                                                                            C;Date: V4 VIIII
C;Accession: I58351
C;Accession: I58351
R;Fox, G.M.; Holst, P.L.; Chute, H.T.; Lindberv
Cncogene 10, 897-905, 1995
A;Title: cDNA cloning and tissue distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R.Slever, D.A.; Verderame, R.Slever, D.A.; Verderame, Gene 148, 219-226, 1994
A;Title: Identification of a complete Cek7
A;Title: number: I50614; MUID:95047429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor-type protein-tyrosine kinase Cek7, long splice form - chicken C;Species: Gallus gallus (chicken) C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 18-Jun-1999 C;Accession: I50615; I50616; I50614
R;Siever, D.A.; Verderame, M.F.
                                                                                                                                                                                                             receptor protein-tyrosine kinase - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                                         RESULT
I58351
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Accession: I50614
A;Accession: I50614
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A;Accession: I50615
A;Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-1013 <SIE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 170
                                                                                                                                                                                                                                                                                                                                                                             257
                                                                                                                                                                                                                                                                                                                                                                                                                     249
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                                                                                                                                                                                                                                                                                                             15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                 preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKEEDPPRMYCSTEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VCNYMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPLVLGTCKETFNLYYMESDD 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLLCAALRS---LLASPGSEVNLLDSRTVMGDLGWIAYPKNGWEEIGEVDENYAPIHTYQ
                                                                                                                                                                                                                                                                                                                                                                          EWLVPIGKCLCKAGYEEKNNTCQ
                                                                                                                                                                                                                                                                                                                                                                                                                   EWLVPIGKCSCNAGYEERGFMCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                           IALVSVRVYYKKCPSVIRNLARFPDTITGADSSQLLEVSGVCVNHSVTDEAPKMHCSAEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                           <RES>
  GB:L36642; NID:g551607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64.68;
                                                                                                                                                                      Chute, H.T.; Lindberg, R.A.; Janssen, A.M.; Basu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                          279
                                                                                                                                                                                                                                                                                                                                                                                                                     271
                                                                 from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  947; DB 2;
No. 4.2e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor protein tyrosine kinase coding
  PIDN:AAA74243.1;
                                                                                                                              of five human EPH-like receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIDN: AAB60612.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIDN: AAB60614.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1013;
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PID: g551608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PID:g555620
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Search completed: May Job time: 4159 sec

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22:27:20

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C;Genetics:
A;Gene: HEKII
C;Superfamily: protein-tyrosine kinase, receptor ty
C;Superfamily: protein-tyrosine kinase, receptor ty
C;Keywords: ATP; transmembrane protein
F;631-897/Domain: protein kinase homology <KIN>
F;639-647/Region: protein kinase ATP-binding motif
F;920-986/Domain: SAM homology <SAM>
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                                                TVKNLAMFPDTVP-MDSQSLVEVRGSCVNNSKE--EDPPRMYCSTEGEWLVPIGKCSCNA 261
                    GYEERGFMCQ 271
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Gapop 10.0 , Gapext 1.0
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Database

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                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 435)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,
Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,
Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,
Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
Wilson,R.
                                                                                                                                                                                                     RECEPTOR HEK PRECUR
H38363
H38363.1 GI:907862
                                                                                                                                                                                                                               H38363 435 bp mRNA EST 16-AUG-1995 yp50g04.rl Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:190902 5' similar to gb:M83941 TYROSINE-PROTEIN KINASE RECEPTOR HEK PRECURSOR (HUMAN); mRNA sequence.
The WashU-Merck EST Project Unpublished (1995)
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AIO11632 ESTZÓ6082
AIO11632 ESTZÓ6083
B36983 HS-1042-A2
AI325344 mIO1CO2.y
AI325344 mIO1CO2.x
AI325334 mIO1CO2.x
AI323334 mIO1CO2.x
AI333334 mIO1CO2.x
AI333334 mIO1CO2.x
AI337308 t1598b01.x
AIVA45288 UI-M-BH1.x
AIVA45288 UI-M-BH1.x
AIVA45288 UI-M-BH1.x
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AIVA4528 UI-M-BH1.x
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AA746914 nx69802.s
AW017395 EST2772817
AW256663 EST304800
AI366919 qv94N06.x
AI143874 qe04f05.x
AI112217 UI-R-Y0-m
AL098595 Drosophil
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            363
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On May 5, 1995 this sequence version replaced gi:797807.
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
Insert Size: 2663
High quality sequence stops: 276
Source: IMAGE Consortium, LINL
This clone is available royalty-free through LLNL; contact the
INAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2663
Std Error: 0.00
Seq primer: M13Rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cactctacgagactgcaatagcattccattggttttaggaacttgcaaggagacattcaa
CACTCTACGAGACTGCAATAGCATTCCATTNGTTTTAGGNACTTNCAAGGGGACATTAAC
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/db_xref="GDB:3847311"
/db_xref="taxon:9606"
/clone="IMAGE:190902"
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/sex="male"
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            atcaggacttaccaggtgtgcaatgtcatggaccacagtcaaaacaattggctgagaaca 252
                                                                                            CCCGCGAATGAAGTTACTTTATTGGATTCCAGATCTGTTCAGGGAGAGCTTGGGTGGATA 194
                                                                                                                                          TTCATCCTCTTTTCGTTTCTCTTTGGAATTTGCGACGCTGTCACCGGTTCTAGGGTATAC 134
                                                                                                                                                                  tccatcctcctcctcagctgctctgttctcgacagcttcggggaactgattccgcag 75
                                                            tcttatccat---cacatgggtgggaagagtcagtggtggtgggtggaacattacacaccc
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Hashimoto, K., Kusuda, J., Toyoda, A., Tanuma, R., Suzuki, Y., Sasaki, M. and Sugano, S.
Isolation of full-length cDNA clones from a moulibrary made by oligo-capping method Unpublished (1999)
On May 18, 1998 this sequence version replaced Contact: Katsuyuki Hashimoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       National Institute of Infectious Diseases 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo: Email: khashi@nih.go.jp
URL: http://www.nih.go.jp/yoken/genbank/.
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l (bases
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                                                                                                                                                                                                                                                                      202
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                 /strain="C57BL"
/db_xref="taxon:10090"
/clone="MNCD-6241"
/clone_lib="Sugano mouse b
/sex="female"
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Rodentia;
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                                                                                                                                               Unpublished (1999)
On Jun 5, 1998 this sequence version
Other_ESTs: fi31g02.x1
Contact: S.L. Johnson
Washington University School of Medic
4444 Forest Park Parkway, Box 8501, 8
                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Releostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Cyprinidae; Rasborinae; Danio.

1 (bases 1 to 572)
1 (bases 1 to 572)
Sugano, S., Kawakami, K., Johnson, S., Li, F., Maxra, M., Eddy, S., Hillier, L., Clifton, S., Allen, M., Gibbons, M., Jost, S., Kucaba, T., Martin, J., Pape, D., Steptoe, M., Underwood, K., Theising, B., Ritter, E., Bowers, F., Wylie, T., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW175051 572 bp mRNA EST 16-NOV-1999 fi31902.yl Sugano Kawakami zebrafish DRA Danio rerio cDNA clone 2639282 5' similar to SW:EPA4_CHICK Q07496 EPHRIN TYPE-A RECEPTOR
                            Email: est@watson.wustl.edu
Library constructed by Dr. Sumio Sugano
Sequencing by: Washington University Gen
Seq primer: T3 ET from Amersham
High quality sequence stop: 485.
                                                                                                                                                                                                                                                            WashU
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Sequencing
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/organism="Danio rerio

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ROVAX55 3' end, mRNA s
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AI011631.1 GI:3225463
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Rattus sp.
Eukaryota;
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/db_xref="taxon:7955"
/clone="2639282"
/clone_lib="Sugano Kawakami zebrafish
/sex="mixed (one male and one female,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unfertilized eggs)"
/dev_stage="adult"
      Metazoa;
                                                                                                                         GI:3225463
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d rat ovary,
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                                                                                                                                    TGAATGTGGAGGAGCGCATGGTGGGGCCCCTTACCCGGAAGGGCTTCTA
                                                                                                                                                   tcaacactgagattagagaagtaggtcctgtcaacaagaagggatttta 539
                                                                                                                                                                                                              acaccattgcagctgatgaaagtttcactcaaaatggatctttggggaccgtattctgaagc 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ccatcaggacttaccaggtgtgcaatgtcatggaccacagtcaaaacaattggctgagaa 250
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                                                                                                                                                                                            ACACCATCGCCCCTGACGAGATCACGGTCAGCAGTGACTTCGAGGCTCGCAATGTCAAGC
                                                                                                                                                                                                                                                                                                                   GAGACTGCAATAGCTTTCCGGGTGGCGCCCAGCTCCTGCAAAGAGACCTTCAACCTCTACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@tigr.org
Seg primer: M13-21.
AI011632 473 bp mRNA
ESTZ66083 Normalized rat ovary
ROYAX56 3' end, mRNA sequence
AI011632
AI011632:1 GI:3225464
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On Jan 19, 1998 this
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria; Rodentia;
1 (bases 1 to 474)
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ilarity 57.1%;
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/db_xref="ARCC (inhost):2021827"
/db_xref="ARCC (inhost):2021827"
/db_xref="taxon:10118"
/clone="ROYAX55"
/clone_Tib="Normalized rat ovary, Bento S
/note="Organ: ovary; Vector: pT7T3Pac; S1
Site_2: NotI"
7 a 129 c 135 g 93 t
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Pred. No. 2.8e-34;
0; Mismatches 201;
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                                           Rattus sp.
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Matches 262; Conserv
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Rattus sp.
Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 473)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quacken
Kerlavage, A.R. and Adams, M.D.
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On Jan 19, 1998 this sequence version
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primer: M13-21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Institute for Genomic Research
Z, Medical Center Drive, Rockville,
: (301)-838-3529
: (301)-838-0208
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/note="Organ: ovary; Vector: pT7T3Pac; Site_1:
Site_2: NotI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Rattus sp."
/db_xref="ATCC (inhost):2021828"
/db_xref="taxon:10118"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="ROVAX56"
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57.3%;
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Pred. No. 1.5e-33;
0; Mismatches 195
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                                                                                                                    gttcctgcaatgctggctatgaagaagaggttttatgtgccaa
                                                                                                                                                                                 aagatcctccaaggatgtactgcagtacagaaggcgaatggcttgtacccattggcaagt 769
                                                                                                                                                                                                                                                 actcccagtccctggtggaggttagagggtcttgtgtgtcaacaattctaagga-----gg 709
                                                                                                                                                                                                                                                                                                                   aaaagtgcccatttacagtgaagaatctggctatgtttccagacacggtacc---catgg 655
                                                                                                                                                                                                                                                                                                                                                                                    atttggcatttcaagatgttggttgcttgtgttgccttggtgtctgtgagagtatacttca 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                   gtattotgaagotcaacactgagattagagaagtaggtoctgtcaacaagaagggatttt 538
                                                                                                   GTATCTGCAAAGCAGGCTACCAGCAAAAAGGAGACACTTGTGAA
                                                                                                                                                                  AAAACGCCCCCAGGATGCACTGCAGTGCAGAAGGAGAATGGTTAGTGCCCATTGGAAAAT
                                                                                                                                                                                                                                 AATTTTCCTCTTTAGTCGAGGTTCGAGGGACATGTGTCAGCAGTGCAGAGGAAGAAGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                 GNATACTCAAGCTTAACACTGAGGTGAGAGAGATTGGACCTTTGTCCAAAAAGGGATTCT 61
                                                                                                                                                                                                                                                                                               AGAAGTGCTGGTCCATTATTGAGAACTTAGCTATCTTTCCAGATACAGTGACTGGTTCAG
                                                                                                                                                                                                                                                                                                                                                                ATCTTGCCTTTCAGGATGTAGGGGCTTGCATAGCTTTGGTTTCTGTCAAAGTGTACTACA 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Mahairas GG, Zackrone University of Washington Seattle, WA 98195, USA Tel: (206) 616-8744 Fax: (206) 685-7301 Email: kzackron@u.washington.ec
   AI325344
mi01c02.y1
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Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
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1 (bases 1 to 424)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Organ: sperm; Vector: pBeloBAC11; BAC
E-Coli DH10B"
1 77 c 101 g 122 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=CT 824 Col=10 Row=K"
/clone_lib="CIT Human Genomic Speri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="M"
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L Soares
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Pred. No. 4.4
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placenta
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Hood,L.E.
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Best Local Similarity
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                                                                                                                                                                                       TACTCGGTGTGCAACGTGGTATCCGGCGACCAGGACCAGCTGGGTGCTACCAACTGGGTG
                                                                                                                   ccatcacatgggtgggaagagatcagtggtgtggatgaacattacacacccatcaggact 201
                                                                                                                                                                AAGGAAGTTGTTTGGTTGGACTTCGCAGCAATGAAGGGAGAGCTCGGCTCGCCTCACGCAC 334
                                    taccaggigigcaatgicatggaccacagicaaaacaatiggcigagaacaaacigggic 261
                                                                                 CCCTATGGCAAAGGGTGGGACCTGATGCAGAACATCATGGACGACATGCCTATCTACATG
                                                                                                                                                                                                                                                   218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            on Jan 19, 1998 this sequence version repl
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. LK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 406)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone IMAGE:459170 5' similar to gb:U07634 Mus musculus receptor-protein tyrosine kinase (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: -40RP from Gibco.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  read is a RESEQUENCE of a previously sequenced mouse clone read has been verified (found to hit its original self in
                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                          79
                                                                                                                                                                                                                                                                                                                                                                T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."

a 117 c 109 g 100 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
lst strand cDNA was primed with a Not I - oligo(dT) primer
[5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:459170"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Soares mouse
/sex="unknown"
                                                                                                                                                                                                                                                                  15.6%;
58.9%;
                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                               Score 126.8; DB 44;
Pred. No. 5.2e-28;
0; Mismatches 152;
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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On Sep 21, 1992 this sequence version replaced
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1 (bases 1 to 402)

1 Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Parsons,J., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yf88e12.rl Soares infant brain 1NIB Homo sapiens cDNA clone IMAGE:99543 5' similar to gb:863941 TYROSINE-PROTEIN KINASE RECEPTOR HEK PRECURSOR (HUMAN); mRNA sequence.
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Location/Qualifiers
                   /db_xref="taxon:9606"
/clone="IMAGE:29543"
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/db_xref="GDB:401890"
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Best Local Similarity
Matches 218; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                     Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                            Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 493)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                            /clone="IMAGE:2004483"
/clone_lib="NCI_CGAP_Pan1"
/tisue_type="adenocarcinoma"
/lab_host="DH10B"
/note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: Sa
Site_2: NotI; Cloned unidirectionally. Primer: Oligo d
Average insert size 1.72 kb. Life Technologies catalog
11548-013"
a 141 c 142 g 101 t 2 others
                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 1.1
                                         Score 112.2; DB 44;
Pred. No. 1.6e-23;
0; Mismatches 159;
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1.1e-25;
hes 84;
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Fax: 314 286 1810
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                                                                                           /organism="Mus musculus"
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/db_xref="taxon:10090"
/clone="IMAGE:459170"
                                     /tissue_type="placenta"
/dev_stage="adult"
                                                                  /sex="unknown"
                                                                              /clone_lib="Soares mouse
                                                                                                                                                                 Location/Qualifiers
                         /lab_host="DH10B"
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AA024123
                                                                                                                                                                                                                                                                                                                                                                         Fax: 314 400 40-0
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On May 8, 1995 this sequence version Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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  /note="Organ: placenta; Vector: pT7T3D-Pac
with a modified polylinker; Site_1: Not I;
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Site_2: Eco
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                                                                                                                                                     on Jan 17, 1998 this sequence version repi
Contact: Marra M/Mouse EST Project
Washingthon University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lc
Tel: 314 286 1800
Fax: 314 286 1810
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1 (bases 1 to 348)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wilie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
                     This clone was previously sequenced on data is from the 3' end
                                                                                                                                                                                                                                                                                                                       Unpublished (1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                    MGI:276058
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103 c 102 g 92 t
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Pred. No. 5.9e-23;
0; Mismatches 98;
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                                                                                                                                                                        A1337308 496 bp mRNA EST 18-MAR-1999 tb98b01.x1 NCI_CGAP_CO16 Homo sapiens cDNA clone IMAGE:2062345 3/ similar to SW:EDB2_HUMAN P29323 EPHRIN TYPE-B RECEPTOR 2 PRECURSOR ; contains element MER22 repetitive element ;, mRNA sequence.
A1337308
                               Eukaryota; Metazoa; Chordata; Craniata; Vertu
Eutheria; Primates; Catarrhini; Hominidae; H
1 (bases 1 to 496)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
                                                                                                                                          EST
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Tumor
                                                                                                                                                           AI337308.1
              National Cancer Institute,
                                                                                                      Homo sapiens
                                                                                                                          human
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Gene Index
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94 c 93 g 74 t
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with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
lst strand cDNA was primed with a Not I - oligo(dT) primer
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/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="IMAGE:459170"
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Location/Qualifiers
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/strain="C57BL/6J"
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                                                                                                                                                           GI:4074235
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                                                                   Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
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Pred. NO. 8e-21;
0; Mismatches 14
              Cancer Genome Anatomy Project (CGAP),
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Best Local Similarity
Matches 204; Conserv
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                                                                                                                                                                                                                                                                                                   actcaaatggatcttggggaccgtattctgaagctcaacactgagattagagaagtaggt 516
                                                                                                                                                                                                                                                                                                                                                                   gtgaaatttcgagagcatcagtttacaaagattgacaccattgcagctgatgaaagtttc 456
                                                                                                                                                                                                                                                                                                                                                                                                                                            aaggagacattcaacctgtactacatggagtctgatgatcatg-----gg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9t9gagctcaagttcactctacgagactgcaatagcattccattggttttaggaacttgc 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGCCAGAACAACTGGCTACGGACCAAGTTTATCCGGCGCGCGTGGCGCCCACCGCATCCAC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agtcaaaacaattggctgagaacaaactgggtccccaggaactcagctcagaagatttat 288
                                                                                                                                                                                                                    cctgtcaacaagaagggattttatttggcatttcaagatgttggtgcttgtgttgccttg 576
                                                                                                                                                                                                                                                                     TCCCAGGTGGACCTGGGTGGCCGCGTCATGAAAATCAACACCGAGGTGCGGAGCTTCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGGAGATGAAGTTTTCGGTGCGTGACTGCAGCAGCATCCCCAGCGTGCCTGGCTCCTGC 130
                                                                                                                       GTGCC
                                                                                                                                                         gtgtc
                                                                                                                                                                                          CCTGTGTCCCGCAGCGGCTTCTACCTGGCCTTCTACTGTAACGGGGACGGCGAGTGGCTG
                                                                                                                                                                                                                                                                                                                                              CCCAACTGGATGGAGAATCCATGGGTGAAGGTGGATACCATTGCAGCCGACGAGAGCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                       AAGGAGACCTTCAACCTCTATTACTATGAGGCTGACTTTGACTCGGCCACCAAGACCTTC 190
AW045268 314 bp mRNA EST 18-SEP-1999
UI-M-BH1-akn-b-03-0-UI.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 479.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insert Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: M. Bento Soares, Ph.D. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                       375
                                                                                                                                                           581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Robert_Strausberg@nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Colo was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1145351).

Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE:2062345"
/clone_lib="NCI_CGAP_Col6"
/tissue_type="colon tumor,
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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55.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 92.6; DB 45;
Pred. No. 1.6e-17;
0; Mismatches 149;
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Best Local S
Matches 164
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MEDLINE
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                                           202
                                                                                                                            142
                                                                                  81
                                                                                                                                                                     21
                                                                                                                                                                                       82 aatgaagtcaatctactggattcaaaaacaattcaaggggagctgggctggatctcttat 141
TACTCGGTGTGCAACGTGGTATCCGGCGACCAGGACAACTGGCTCCGCACCAACTGGGTG
                     taccaggtgtgcaatgtcatggaccacagtcaaaaccaattggctgagaacaaactgggtc 261
                                                                              CCCTATGGCAAAGGGTGGGACCTGATGCAGGACATCATGGACGACATGCCTATCTACATG 140
                                                                                                                     ccatcacatgggtgggaagagatcagtggtgtggatgaacattacacacccatcaggact 201
                                                                                                                                                               164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIH BMAP cDNA clones will be made available by the means that is soon to be determined. When NIH determines the means for distribution of the BMAP cDNA clones, this record will be updated accordingly when that means is determined.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mEST@mail.nih.gov
Oligo-dT track not found, Not I si
is likely internal to the message.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 301 443 1706
Fax: 301 443 9890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq primer: Ml3 Forward POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6001 Executive Blvd. 20892-9643, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Chin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Jun 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97044477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two approaches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW045268.1 GI:5905797
EST.
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                                                                                                                                                                                                                                                                        Similarity
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(bases 1 to 314)
                                                                                                                                                                                                                                                                                                                                                                                72
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          olfactory bulbs, hypothalamus, cortex, amygdala, basal ganglia, pineal gland, striatum, hipoccampus). The driver used for subtraction consisted of a pool of 5,000 clones from the NIH_BMAP_M_S1 library and a pool of 2,000 clones obtained from non-normalized and normalized mouse brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /lab_host="DH108 (Life Technologies)"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The NIH_BMAP_M_S2 library is a subtracted library derived find the subtracted library derived find the subtracted library derived from a mixture of normalized libraries from ten
                                                                                                                                                                                                                                                                                                                                                                              TAG_SEQ=CATGG"
84 c
                                                                                                                                                                                                                                                                                                                                                                                                                     TAG_TISSUE-olfactory-bulbs
                                                                                                                                                                                                                                                                                                                                                                                                                                         Spinal cord libraries. TAG_LIB-NIH_BMAP_M_S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regions of the mouse brain (cerebellum, brain stems,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="UI-M-BH1-akn-b-03-0-UI"
/clone_lib="NIH_BMAP_M_S2"
/dev_stage="27-32 days"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism-"Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metazoa;
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                                                                                                                                                                                                                                                Score 89; DB 64;
Pred. No. 1.7e-16;
D; Mismatches 126
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                                                                                                                                                                                                                                                    126;
                                                                                                                                                                                                                                                                                         Length 314;
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Matches 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262
                                                                                                                                                         Local Similarity
acagtgaagaatctggctatgtttccagacacggtacccatggactcccagtcc---ctg
                                                                          agcattccattggttttaggaacttgcaaggagacattcaacctgtacta 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cccaggaactcagctcagaagatttatgtggagctcaagttcactctacgagactgcaat
                                               GACATAGGTGCCTGCCCTGGCCATCCTCTCTCTCCGCATCTACTATAAGAAGTGCCCTGCC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCTTCCCGGGTGGCGCCAGCTCATGCANAGAGACCTTCAACCTCTACTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
Unpublished (1997)
On Jun 5, 1998 this sequence version replaced gi:3189146.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 418)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D.,
R. Emmert-Buck, M.D., Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seq primer:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA Library Preparation: M. Bento Soares, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA sequence.
                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                   Bento Sc
152 c
                                                                                                                                                                                                                                                            polylinker; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDS 1257096-125863), 1459064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="IMAGE:2516671"
/clone_lib="NCI_CGAP_GC6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note "Vector: pT7T3D-Pac (Pharmacia) with a modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
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Location/Qualifiers
                                                                                                                                                       10.8%;
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                                                                                                                                Score 88.2; DB 63;
Pred. No. 3.3e-16;
0; Mismatches 88;
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KEYWORDS
SOURCE
ORGANISM
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Best Local S
Matches 143
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TITLE
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                    182 attacacacccatcaggacttaccaggtgtgcaatgtcatggaccacagtcaaaacaatt 241
                                                                      Local Similarity 60.1
mes 143; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=ILO&t2=ILO-HT0156-
251099-132-al2&t3=1999-10-25&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
On Mar 16, 1998 this sequence version replaced g1:2961824.
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ILO-HT0156-251099-132-a12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The FAPESP/LICR Human Cancer Genome Project
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3P http://www.ludwig.org.br/ORESTES.
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                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/dev_stage="Adult"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."
73 a 98 c 95 g 78 t
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                                                                                     10.6%;
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; Pred. No. 1.4e
0; Mismatches
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                                                            DB 80; L. 1.4e-15; 95;
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                                                                                                        Length 344;
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Result
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Listing first 45 summaries
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1: /cgn2_6/ptodata/

2: /cgn2_6/ptodata/

3: /cgn2_6/ptodata/

4: /cgn2_6/ptodata/

5: /cgn2_6/ptodata/

6: /cgn2_6/ptodata/

7: /cgn2_6/ptodata/
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/5D_COMB.seq:*
/cgn2_6/ptodata/2/ina/6_COMB.seq:*
/cgn2_6/ptodata/2/ina/FCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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        GenCore version 4.5 (c) 1993 - 2000 Com
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   US-08-167-919A-9
US-08-162-809-15
US-08-469-537A-102
US-08-449-537A-102
US-08-449-645A-14
US-08-449-645A-14
US-08-673-78-10
US-08-673-78-10
US-08-673-78-10
US-08-673-78-10
US-08-678-16-34
PCT-US95-04281-14
US-08-702-367A-16
PCT-US95-04281-16
US-08-449-645A-16
US-08-449-645A-16
US-08-68-702-367A-16
PCT-US95-04681-11
US-08-162-809-19
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US-08-162-809-17
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Sequence 9, Appli
Sequence 15, Appli
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Sequence 102, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 110, Appli
Sequence 14, Appli
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US-08-167-919A-9
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80.8	80.8	80.8	80.8	115.4	136	136	136	136	136	136	141.4	150	150	194.4	194.4	194.4	213.4
9.9	9.9	9.9	9.9	14.2	16.7	16.7	16.7	16.7	16.7	16.7	17.4	18.5	18.5	23.9	23.9	23.9	26.2
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PCT-US95-04228-23	US-08-436-054-5	US-08-222-616-23	US-08-436-044-5	US-08-162-809-1	US-08-571-785-4	US-08-571-785-3	US-08-348-143-4	US-08-348-143-3	US-08-571-785-2	US-08-348-143-2	US-08-162-809-7	US-08-162-809-13	US-08-162-809-9	PCT-US95-04681-10	US-08-702-367A-10	US-08-449-645A-10	US-08-162-809-11
Sequence 23, Appl	Sequence 5, Appli	Sequence 23, Appl	Sequence 5, Appli	Sequence 1, Appli	Sequence 4, Appli	Sequence 3, Appli	Sequence 4, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 7, Appli	Sequence 13, Appl	Sequence 9, Appli	Sequence 10, Appl	Sequence 10, Appl	Sequence 10, Appl	Sequence 11, Appl

ALIGNMENTS

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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Vers
SOSTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,919A
FILING DATE: 18-APR-1994
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-UN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK9992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-UN-1992
APPLICATION NUMBER: 9X394
APPLICATION NUMBER: 31,346
FILING DATE: 19-UN-1992
ATTONNEY/ACENT INFORMATION:
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9159
TELEPHONE: (516) 742-4343
TELEPHONE: (516) 742-4343
TELEPHONE: 320,012 Number: 320,012 Number:
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CORRESPONDENCE ADDRESS:
    SEQUENCE CHARACTERISTICS:
LENGTH: 3132 base pair
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MEDIUM TYPE: Floppy disk
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STATE: New York
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Ward, Larry D.
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TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
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         gctggctatgaagaaagaggttttatgtgccaa 813
                                          aggatgtactgcagtacagaaggcgaatggcttgtacccattggcaagtgttcctgcaat
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                                AGGATGTACTGCAGTACAGAAGGCGAATGGCTTGTACCCATTGGCAAGTGTTCCTGCAAT
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100.0%; Pred. No. 2.9e-253;
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RESULT 2 US-08-715-106-9 ; Sequence 9, Application

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US-08-715-106-9
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TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3132 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
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Best Local Similarity
Matches 813; Conserv
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION UNMER: US/08/715,106
FILING DATE: 18-SEP-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/167,919
FILING DATE: 18-APR-1994
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION UNMER: PK9992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 911
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: D1G1g110, Frank S.
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Boyd, Andrew W. APPLICANT: Simpson, Richar APPLICANT: Wicks, Ian
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GAGCTGGGCTGGATCTCTTATCCATCACATGGGTGGGAAGAGATCAGTGGTGTGGATGAA
                                                                       GAACTGATTCCGCAGCCTTCCAATGAAGTCAATCTACTGGATTCAAAAACAATTCAAGGG
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RESULT 3
US-08-162-809-15
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          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,809
FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                         APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS (
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
  ATTORNEY/AGENT INFORMATION:
                                                                                                   ADDRESSEE: CAMPB.
STREET: 4370 La.
CITY: San Diego
STATE: Californi.
COUNTRY: United.
ZIP: 92122
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STRANDEDNESS:
FEATURE:
NAME/KEY: CDS
LOCATION: 32...
US-08-162-809-15
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                        acagtgaagaatctggctatgtttccagacacggtacccatggactcccagtccctggtg
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agtacagaaggcgaatggcttgtacccattggcaagtgttcctgcaatgctggctatgaa
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Pred. No. 1.4e-166;
0; Mismatches 160;
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US-08-469-537A-102
                                                                                                                                                                                Query Match
Best Local Similarity
Matches 512; Conserv
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MEDIUM TYPE: DISARctte
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VETSION 2.0
CURRENT APPLICATION NDATA:
APPLICATION UNMBER: US/08/469,537A
FILING DATE: 06-JUN-1995
CLASSIFICATION DATA:
APPLICATION UMBER: USSN 08/406,247
FILING DATE: 17-MAR-1995
FILING DATE: 17-MAR-1995
FILING DATE: 17-MAR-1995
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APPLICANT: Maison
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: USSN 08/144,992
FILING DATE: 28-OCT-1993
APPLICATION NUMBER: USSN 07/736,559
FILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Ph.D., Gail M
REGISTRATION NUMBER: 32,143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Maisonpierre, et
TITLE OF INVENTION: EHK AND
TITLE OF INVENTION: KINASES
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CORRESPONDENCE ADDRESS:
                                                                                                                 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: REFERENCE/DOCKET NUMBER: REFELECOMMUNICATION INFORMATION: TELEPHONE: 914-345-7400
TELEFAX: 914-345-7721
                    176
                                                  690
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CITY: Tarrytown
STATE: NY
                                                                                                                                                                                                                                                                                                                                                            LENGTH: 3906 base pairs TYPE: nucleic acid STRANDEDNESS: unknown
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                                               TCCGGACCCTTTTGGCCAGCCCAGTAACGAAGTGAATTTATTGGATTCGCGCACTGTCC
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Conservative
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Pred. No. 6.7e-104;
0; Mismatches 246;
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APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,24
FILING DATE: 15-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/3:
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Timothy E
                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
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                                                                                                CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                               STATE:
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IT: 460 Point San Bruno
South San Francisco
                                                                                                                                                                                                                                                                           94080
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REFERENCE/DOCKET NUMBER: 920C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/25-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4165 bases
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Best Local Similarity
Matches 512; Conserv
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STRANDEDNESS: single
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                     cctgcaatgctggctatgaagaagaggttttatgtgccaa 813
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TGTGCAAGGCCGGATATGAAGAGAAAAATGGTACCTGTCAA 1455
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                                                                 ATCCTCCCAAAATGCATTGCAGTGCTGAAGGGGAGTGGCTGGTTCCCATCGGGAAATGCA 1414
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Pred. No. 6.9e-104;
0; Mismatches 246;
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TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4165 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 67.3
Matches 512; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application Patent No. 5798448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible operating SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,815
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330128
FILING DATE: 27-OCT-1994
ANTORNEY/AGENT INFORMATION:
NAME: TOTChia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 920C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
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STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                               56 tcggggaactgattccgcagccttccaatgaagtcaatctactggattcaaaaaacaattc 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: singl
TOPOLOGY: linear
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                                                           cattcaacctgtactacatggagtctgatgatgatcatggggtgaaatttcgagagcatc
                                                                                                             TCAAGTTTACTCTGAGGGATTGCAACAGCCTTCCTGGAGGACTGGGGGACTTGCAAGGAGA
                                                                                                                                      tcaagttcactctacgagactgcaatagcattccattggttttaggaacttgcaaggaga 355
                                                                                                                                                                                    ATAATTGGCTGTTGACCAGTTGGATCTCTAACGAAGGTGCTTCCAGAATTTTTATTGAAC
                                                                                                                                                                                                            acaattggctgagaacaaactgggtccccaggaactcagctcagaagatttatgtggagc 295
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                                                                                                                                                                                                                                                                                                                                   TCCGGACCCTTTTGGCCAGCCCCAGTAACGAAGTGAATTTATTGGATTCGCGCACTGTCC 754
                                    CCTTTAACATGTATTATTTTGAGTCGGATGATGAGAATGGGGAGAATATCAAAGAGAACC
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Pred. No. 6.9e-104;
0; Mismatches 246;
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US-08-673-789-1
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APPLICANT: ZHOU, RENI
APPLICANT: T; KROME:
APPLICANT: GEORGE, F
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/177,81
FILING DATE: 04-CAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPHONE: (212) 751-6849
                                                          TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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STREET: 34
CITY: NEW
STATE: NEW
                         LENGTH:
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         STRANDEDNESS:
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345 PARK AVENUE
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T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEORGE, F
         DOUBLE
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US-08-469-537A-100
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               GEMERAL INFORMATION:
APPLICANT: Maisomplerre, et a
TITLE OF INVENTION: EHK AND R
TITLE OF INVENTION: KINASES
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharma
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Best Local S
Matches 511
                                                                                                                                               Sequence 100, Application Patent No. 5843749
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Regeneron Pharmaceuticals, 7 Old Saw Mill River Road
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Pred. No. 2.3e-103;
0; Mismatches 247;
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Best Local :
                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3592 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: USSN FILING DATE: 26-JUL-1991 ATTORNEY/AGENT INFORMATION: NAME: Kempler, Ph.D., Ga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/469
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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LOCATION:
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APPLICATION NUMBER: USSN
FILING DATE: 28-OCT-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: USSN 08/406,247 FILING DATE: 17-MAR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
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                                                                                                                                                                                                                      Local Similarity
                                                                                                                  gtccccaggaactcagctcagaagatttatgtggagctcaagttcaactctacgagactgc 318
                                                                                                   TATCCACTGAATGGGTGGGATGCCATTACTGAAATGGATGAACACAACAGGCCCATACAT
                                                                                                                                                    TCCAACCAAGTTGTGTTGCTTGATACATCTACAGTGATGGGAGAACTAGGATGGAAAACA 747
ATCTCTCGTGATGCTCAGAAAATCTATGTGGAAATGAAGTTCACATTGAGAGATTGT
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/label= N
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Sequence 14, Application Patent No. 5981245; Patent No. 5981245; GENERAL INFORMATION:
APPLICANT: FOR STANFOLD CONTROL OF THE PATENTIAN CALL OF THE PATENTI
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MOLECULE FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 3116 base pair
                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                    TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 1840 Dehavilland
CITY: Thousand Oaks
STATE: California
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o. 5981245
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; Sequence 14, Application US/08702367A
Patent No. 5981246
; GENERAL INFORMATION:
APPLICANT: FOX, GATY M.
TITLE OF INVENTION: EPH-Like Recept
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
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Patent Operations/RBW
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Pred. No. 1.1e-101;
0; Mismatches 231;
                                         Receptor
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NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 3116 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
LOCATION: 34..2994
US-08-702-367A-14
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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CITY: Thousand Oak:
STATE: California
COUNTRY: USA
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FILING DATE:
CLASSIFICATION: 435
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Pred. No. 1.1e-101;
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Best Local Similarity
Matches 509; Conserv
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NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A.
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04681
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TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 91320
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Pred. No. 1.1e-101;
0; Mismatches 231;
                                                                                                                                                                                                                                                                                                                      Length 3116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 K
COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-D

SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT//
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/8:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST TITLE OF INVENTION: ANTIBODIES NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
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                                                                                         APPLICATION NUMBER: US/08/222,616 FILING DATE: 4-APR-1994 CLASSIFICATION: 530
                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
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Goeddel,
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SEQUENCE CHARACTERISTICS:
LENGTH: 3348 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 42.4%;
Best Local Similarity 68.2%;
Matches 509; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 82:
REFERENCE/DOCKET NUMBER: 82:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/92-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
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              atgaagaaagaggttttatgtgccaa 813
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ATGAGGAGCGGAGCGAGAATGCCAA
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Pred. No. 1.1e-101;
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822
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3348 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-04228-34
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PCT-US95-04228-34
Sequence 34, Application PC/TUS9504228
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  Matches 509;
                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION UMBER: 08/222616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 460 Point San Bruno B. CITY: South San Francisco STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb flog
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATIO DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04228
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APPLICANT:
APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/255-1994
TELEPAX: 415/952-9881
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APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 45
                   311
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gagactgcaatagcattccattggttttaggaacttgcaaggagacattcaacctgtact
                                                                        caaactgggtccccaggaactcagctcagaagatttatgtggagctcaagttcactctac 310
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                                                    CTGATTGGATCACCCGAGAAGGGGCTCAGAGGGTGTATATTGAGATTAAATTCACCTTGA 316
                                                                                                                      TAGCAAGCCCTCTGGAAGGAGGGGGGGGAGGAAGTGAGTATCATGGATGAAAAAAATACAC 196
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Goeddel, David
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Pred. No. 1.1e-101;
0; Mismatches 231;
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RESULT 14
US-08-449-645A-16
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                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERRINGE/DOCKET NUMBER: A-2
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 4529 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16, Application Patent No. 5981245 GENERAL INFORMATION:
                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com
                                       TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Lik
TITLE OF INVENTION: Kinases
                            FEATURE:
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CITY: Thousand Oaks
STATE: California
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Sequence 16, Application US/0870236
Patent No. 5981246
GENERAL INFORMATION:
APPLICANT: FOX, GATY M.
TITLE OF INVENTION: EPH-Like Re
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
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                          ADDRESSEE:
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FEATURE:

NAME/KEY: CDS

LOCATION: 186..3182

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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,367A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter; Robert B.
REFERENCE/DOCKET NUMBER: A-287
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
**ENGTH. 459 hase balis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TENGTH: 4529 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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                                                        ttacagtgaagaatctggctatgtttccagacacggtacc---catggactcccagtccc
                                                                                                   AGGATGTAGGGGCTTGCATAGCTTTGGTTTCTGTCAAAGTGTACTACAAGAAGTGCTGGT
                                                                                                                        aagatgttggtgcttgtgtgtgccttggtgtctgtgagagtatacttcaaaaagtgcccat
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                                 CCATTATTGAGAACTTAGCTATCTTTCCAGATACAGTGACTGGTTCAGAATTTTCCTCTT
                                                                                                                                                                       TTAACACTGAGGTGAGAGAGTTGGACCTTTGTCCAAAAAGGGATTCTATCTTGCCTTTC
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                                                                                            GGATGCACTGCAGTGCAGAAGGAGAATGGTTAGTGCCCATTGGAAAATGTATCTGCAAAG 984
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Search completed: May Job time: 4420 sec 15, 2000, 12:05:01

Title: Perfect score:

US-09-104-340-5 813 1 atggattgtcagct

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Sequence:

Scoring table:

IDENTITY_NUC Gapop 10.0 ,

10.0 , Gapext 1.0

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Copyright

GenCore version (c) 1993 - 2000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                 Mouse Nuk tyrosine Eph-related PTK Ce Eph-related PTK Ce EPH-like receptor Eph-related PTK Ce Eph-related PTK Ce Human embryonal ki Eph-related PTK Ce Protein p140 cDNA
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07-JAN-1993.
19-JUN-1992;
12-JUN-1991;
12-DEC-1991;
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Key
5'utr
                   Claim 6; Fig 1; 58pp; English.

This sequence encodes human eph/elk-like kinase (HEK). HEK is expressed in both pre-B cells and T cell lines and in a number of tumours of human origin, eg. lymphoid tumours LKG3, Lila-1 and JM, and the epithelial tumour HeLa. This receptor-type thymidine kinase (TK) and/or its ligands are useful as agents in modulation of the production and/or function of pre-B, B and T cells. The TK and its analogues have activity in transducing signals or in stimulating cellular responses such as growth and/or differentiation.

Sequence 3132 BP; 888 A; 711 C; 759 G; 774 T;
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Q34513;
24-MAY-1993 (first entry)
                                                                                                                                  therapy etc.
Claim 6; Fig 1; 58pp;
                                                                                                                                                         Receptor-type tyrosine kinase reactive with monoclonal antibody III-A4 - is EPH-ELK-like kinase, useful for phosphorylating proteins in modulating pre-B, B and T cell function, in cancer
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Boyd AD, Simpson R, Ward LD,
WPI: 93-036373/04.
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Receptor type tyro
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Result No.

Score

Match

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Query Match 100.0%; Best Local Similarity 100.0%; Matches 813; Conservative 0

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Mismatches

Score 813; DB 1; Pred. No. 6.9e-259;

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Post-processing:

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hits satisfying chosen parameters:

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Eph-related PTK Cek4.
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prognosis; ss.
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              Location/Qualifiers 32..2980 /*tag= a
                                   tyrosine-kinase;
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(LJOL-) LA JOLLA CANCER F
Pasquale EB, Sajjadi FG;
PBS 215256/28.
WPI; 95-215256/28.
P-PSDB; R75711.
Eph-related protein tyroscancer.
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Probes derived from the EPH-related PTKs Cek4 (Q90659) and Ce (Q90660) were used to isolate novel CDNA clones (Q90652-58, Q90661-62) from chicken embryo and embryonic brain libraries. Cek4 is highly expressed in the chicken developing brain and embryonic tissues, as well as in the adult brain and retina. Sequence 3254 BP; 926 A; 737 C; 796 G; 795 T;
                                              atcaggacttaccaggtgtgcaatgtcatggaccacagtcaaaacaattggctgagaaca
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17-MAR-1995; US-406247.
26-JUL-1991; US-736559.
28-OCT-1993; US-144992.
06-JUN-1995; US-469537.
(REGE-) RECENERON PHARM INC.
Maisonpierre PC, Masiakowski P,
PPSDB; W83147.
                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes nucleic acid molecules for ror-1, ror-2, ehk-1 and ehk-2. Also described are the corresponding prot Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor tyrosine kinases. The present sequence encodes rat Ehk-1. Sequence 3906 BP; 1097 A; 876 C; 990 G; 943 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteins
Claim 5; Fig 22; 194pp; English.
Claim 5; Fig 22; 194pp; English.
Claim 5; Fig 22; 194pp; English.
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Rat receptor tyrosine kinase Ehk-1 encoding DNA.
Receptor tyrosine kinase; Ror-1; Ror-2; Ehk-1; Ehk-2;
neurotrophin activity; trkB; proto-oncogene; tyrosine
binding protein; BDNF; NT-3; diagnosis; ss.
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                                                                                                                                                                                                                                                                                       tcggggaactgattccgcagccttccaatgaagtcaatctactggattcaaaaacaattc
ACCGGGTCATGAAGCTGAATACGGAGGTCAGAGATGTAGGACCTCTGAGCAAAAAGGGAT
                                             AGTACATCAAGATCGATACCATTGCTGCTGATGAGAGCTTCACCGAACTTGACCTTGGAG
                                                                                           CCTTTAACATGTATTATTTGAGTCGGATGATGAGAATGGGAGAAATATCAAAGAGAACC
                                                                                                                                                                                                                                        ATGAAAACTATGCCCCCATCCACACCTATCAAGTGTGCAAAGTTATGGAACAGAATCAGA
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O; Mismatches
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. No. 4.5e-106;
ismatches 246;
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1-1; Ehk-2;
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Query Match
Best Local Similarity
Matches 512; Conser

Conservative

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Score 351.4; DB 1; Pred. No. 4.7e-106; D; Mismatches 246;

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AL-1 neurotrophic factor, an eph-tyrosine kinase ligand - used in treatment and diagnosis of neuronal disorders and repartment and diagnosis of neuronal disorders and analysis - related conditions.

Example 1; Page 47-49; 75pp; English.

A CDNA clone (T18893) codes for rat REK7 (R97853), an eph-related tyrosine kinase receptor, for which AL-1 (see also W97854) is a CL ligand. It was isolated using degenerate receptor tyrosine kinase primers (T18894-96) to amplify cDNAs of an adult mouse hippocampal CDNA library. A PCR fragment was used as a probe to isolate the full-length REK7 cDNA from a rat hippocampal cDNA library. An PCR Fragment was used cell lines for surface expression of REK7-binding activity. Primers based on isolated CLDNA, and an amplified fragment was used to screen a human foetal CCLDNA, and an amplified fragment was used to screen human foetal cDNA library, leading to the isolation of AL-1 cDNA (T18897). So Sequence 4165 BP; 1157 A; 907 C; 1035 G; 1066 T;
                                                                                                                                                                                                                                                                                         W09613518-A1.
09-MAY-1996, U14016.
26-OCT-1995, U14016.
27-OCT-1994, US-330128.
07-JUN-1995, US-486449.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus
Key
cds
                                                                                                                                                                                                                                   Caras iW, Winslow WPI; 96-239448/24. P-PSDB; R97853.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat
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T18893;
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V58192
ID 192
ID 22
ID 2
                  US5814479-A.
29-SEP-1998.
11-JUN-1996; 673789.
04-JAN-1994; US-177812.
11-JUN-1996; US-673789.
                                                                                                                                                                                                                                              25-NOV-1998 (first entry)

Mouse Bsk receptor-like tyrosine kinase cDNA clone.

Mouse; Bsk; receptor-like tyrosine kinase; brain; diagnosis; neopla:

Mouse; Bsk; receptor-like tyrosine kinase; brain; diagnosis; neopla:

neurodegenerative disease; limbic system neuron regeneration;

chromosomal abnormality; degenerative growth; development disorder;

viral infection; bacterial infection; Alzheimer's disease; epilepsy

schizophrenia; stroke; cerebral ischaemla; ds.
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V58192;
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(WOUD/) WOUDE G F V.
(ZHOU/) ZHOU R.
Kromer LF, Schulz NT, N
WPI; 98-541751/46.
P-PSDB; W71628.
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The present sequence encodes mouse Bsk, which is a receptor-like tyrosine kinase. The nucleic acid sequence encoding Bsk can be used in Bsk nucleic acid probes, which can be used in detecting alterations in the level of Bsk messenger-RNA (mRNA) in biological samples isolated from a mammal afflicted with a disease, such as neurodegenerative diseases or disorders and neoplasms. The nucleic acid sequence can also be delivered into the limbic system of patients with limbic system neurodegenerative disease, disorder or injury, to promote or enhance limbic system neuron regeneration or growth. Such neurodegenerative disease include, chromosomal abnormalities, degenerative growth and development disorders, viral infections, bacterial infections, brain injuries, neoplastic conditions, Alzheimer's disease, epilepsy, schizophrenia, or stroke and cerebral ischaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 43.9
Best Local Similarity 67.3
Matches 511; Conservative
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R 28-OCT-1993; US-736559.
R 28-OCT-1993; US-144992.
R 06-JUN-1995; US-469537.
REGENERON PHARM INC.
MAISONDIETTE PC, MASIAKOWSKI P P-PSDB; W83148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUN-1995;
17-MAR-1995;
26-JUL-1991;
28-OCT-1993;
06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                             proteins Claim 7;
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The present invention describes nucleic acid molecules for ror-1, ror-2, ehk-1 and ehk-2. Also described are the corresponding prot Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor tyrosine kinases. The present sequence encodes rat Ehk-2. Sequence 3592 BP; 946 A; 916 C; 894 G; 834 T;
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Rattus s
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Rat receptor tyrosine kinase Ehk-2 encoding DNA.
Receptor tyrosine kinase; Ror-1; Ror-2; Ehk-1; Ehk-2; neurotrophin activity; trkB; proto-oncogene; tyrosine binding protein; BDNF; NT-3; diagnosis; ss.
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tctgatgatgatcatggggtgaaatttcgagagcatcagtttacaaagattgacaccatt 438
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Query Match Best Local Sin Matches 509;

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Score 344.4; DB 1; Pred. No. 8.3e-104; D; Mismatches 231;

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PT or prodn.

PS Claim 1; Page 57-62; 133pp; English.

CC cDNAs (702946-49) coding for 4 novel human EPH-like receptor protein CC tyrosine kinases, HEK5, HEK7, HEK8 and HEK11 (R85089-92), respectively, CC were isolated from a human foetal brain cDNA library using a directed CC PCR approach with primers (see T02960-61) based on conserved regions of CC receptor PTKS and EPH-like receptor PTKS. HEX5, HEX7 and HEX8 show extensive homology to the catalytic domain of chicken EPH-like receptors. The isolated cDNAs are used for prodn. of CEPH-like receptor. The isolated cDNAs are used for prodn. of recombinant HEKS and chimeric receptors, in hybridisation assays, and to detect abnormalities in HEK receptor genes.

SQ Sequence 3116 BP; 859 A; 720 C; 812 G; 725 T;
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WPI; 95
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12-OCT-1995; U04228.
04-APR-1995; U04228.
04-APR-1994; US-222616.
(GETH ) GENENTECH INC.
Bennett BD, Goeddel D,
                                                                                                                                                                                           Protein tyrosine-kinase bpTK7
Protein tyrosine-kinase; pTK;
differentiation; ss.
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VI Wood WI;

R WPI; 95-366160/47.

R P-PSDB; R85936.

PT Agonist antibodies which activate specific protein tyrosine
PT Agonist antibodies which activate chimeric proteins of kinase extracellular
PT Agonist antibodies which activate chimeric proteins of kinase extracellular
PT domain and Ig constant domain, useful for studying, and therapeutic
PT modulation of, cell growth and differentiation
PS Disclosure; Page 88-92; 125pp; English
CC DNA probes based on protein tyrosine-kinase (pTK) sequences were used
CC to screen cDNA libraries to identify novel pTK genes. The bpTKs,
CC bpTKl, bpTK2, bpTK3, bpTK4, bpTK5 and bpTK7 (R85924-28 and R85935,
CC respectively) are expressed in human brain tissue and show homology
CC to known pTKs. A full-length sequence for the bpTK7 gene (T03100)
CC was obtd. This gene may be used to design new drugs, peptides and
CC antisense constructs that modulate pTK activity.
SQ Sequence 3348 BP; 924 A; 769 C; 855 G; 800 T;
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Pred. No. 8.6e
0; Mismatches
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1.6e-104;
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Best Local S
Matches 512
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Sequence 4529 BP; 1449 A; 834 C; 1000 G; 1246 T;
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Claim 1; Page 66-71; 133pp; English.
CDNAs (T02946-49) coding for 4 novel
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P-PSDB; R85092
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EPH-11ke receptor protein tyrosine kinase HEK11
EPH-11ke receptor protein tyrosine kinase; PTK;
human eph-11ke kinase; therapy; diagnosis; antil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid encoding EPH-like receptor tyrosine kinase(s) - and related vectors, host cells, proteins, antibodies etc., used diagnostically and therapeutically to modulate receptor activation
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16-APR-1996
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3M, Jing S, Welcher
95-373799/48.
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tcaacactgagattagagaagtaggtcctgtcaacaagaagggattttatttggcatttc
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No. 1e-103;
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Best Local S
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Or prosent prodn.

Or prosent primers (see T02960-61) based on conserved regions of receptor PTKs and EPH-like receptor PTKs.

HEKT, HEKT, and HEKB show receptors.

Or prodn.

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Or protein

Or proserved regions of receptor PTKs.

HEKT, HEKT, and HEKB show receptors.

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WPI; 95
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                                                                                                                                                                                                                                                                                                 to detect abnormalities in HEK receptor genes. Sequence 3162 BP; 921 A; 667 C; 775
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15-APR-1994;
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95-373799/48.
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S, Welcher
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Pred. No. 1.8e-103;
0; Mismatches 251;
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W09621013-A1.
11-JUL-1996; U00419.
03-JAN-1995; US-368776.
(PLAC) MAX PLANCK GES F
(SUGE-) SUGEN INC.
                                                                                                                                                              11-NOV-1996 (first entry)
Mouse developmental kinase 1; MDK1 T2; receptions of transduction; probe; diagnosis; neurodegeneration; neuroproliferation; cance
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233. 316
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CDNA cloning using adult mouse brains and MDK1 T2 (T32962), that coded for truncated versions (M03422 and M03423, respectively) of the novel mouse developmental kinase 1 (MDK1) (see also T32960), a new member of the eck/eph family of receptor tyrosine kinases.

MDK T1 and T2 each possess the entire ectodomain, the transmembrane domain and part of the juxtamembrane region of MDK1 (see also W03421), but lack the catalytic tyrosine kinase domain. They may have a modulatory function. The CDNA clones can be used to produce MDK1 T1 and T2, which are useful for screening potential agents for treatment of diseases characterised by abnormal signal transduction. Sequence 2323 BP; 680 A; 497 C; 609 G; 537 T;
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GAATGCATTGCAGTGCAGAAGGAGGGGGTAGTACCCATTGGAAAATGCATCTGCAAAG
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03-JAN-1995; US-368776.
(PLAC) MAX PLANCK GES FO (SUGE) SUGEN INC.
Clossek T, Millauer B,
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CDNA cloning using adult mouse brains and Northern blotting dentified 2 clones, MDK1 T1 (T32961) and MDK1 T2 (T32962), that coded for truncated versions (W03422 and W03423; respectively) of the novel mouse developmental kinase 1 (MDK1) (see also T32960), a new member of the eck/eph family of receptor tyrosine kinases.

MDK T1 and T2 each possess the entire ectodomain, the transmembrane domain and part of the juxtamembrane region of MDK1 (see also W03421), but lack the catalytic tyrosine kinase domain. They may have a modulatory function. The cDNA clones can be used to produce MDK1 T1 and T2, which are useful for screening potential agents for treatment of diseases characterised by abnormal signal transduction. Sequence 2901 BP; 890 A; 578 C; 650 G; 783 T;
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Mouse developmental kinase 1; MDK1 T1 clone.
Mouse developmental kinase 1; MDK1 T1; rece
RTK; signal transduction; probe; diagnosis;
neurodegeneration; neuroproliferation; canc
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T32961;
11-NOV-1996 (fi)
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Pred. No. 1.2e-100;
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be; diagnosis; gene therapy;
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03-JAN-1996; U00419.
03-JAN-1995; US-368776.
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C10SSEK T, Millauer B,
WPF; 96-33398/33.
P-PSDB; W03421.
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Mouse developmental kinase 1; MDK1; receptor tyrosine
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08-JUN-1995.
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Novel EPH-related PTK cDNA clone Cek7 (given in 090653) and its variant Cek7+ (090661) were isolated from a chick embryo library in lambda gtl1, and another variant, Cek7' (090662), from a chick embryonic brain cDNA library in lambda gtl1. The variants may originate via alternative splicing of the same gene. Cek7 had the lowest level of expression of 7 novel Eph-related kinases examined and was barely detectable in adult tissues.

Sequence 3056 BP; 871 A; 661 C; 762 G; 762 T;
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P-PSDB; R75714
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08-JUN-1995.
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(LOCL-) LA JOLLA CANCER RES
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Cek7; Eph; protein tyrosine kinase;
prognosis; ss.
Gallus sp.
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Claim 2; Page 44-47; 129pp; English.

Novel EPH-related PTK cDNA clone Cek7 (given in Q90653) and its variant Cek7+ (Q90661) were isolated from a chick embryo library in lambda gtl1, and another variant, Cek7' (Q90662), from a chick embryonic brain cDNA library in lambda gtl1. The variants may originate via alternative splicing of the same gene. Cek7 had the lowest level of expression of 7 novel Eph-related kinases examined and was barely detectable in adult tissues.

Sequence 3059 BP; 860 A; 632 C; 758 G; 809 T;
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WPI; 95-215256/28.
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1 (bases 1 to 3132)

Boyd, A.W., Simpson, R. John, Wicks, I., Method of screening for ligands to a Patent: US 5674691-A 9 07-OCT-1997;

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                    Unknown
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Pred. No. 4.3e-241;
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                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3149)

Wicks,I.P., Wilkinson,D., Salvaris,E. and Boyd,A.W.

Molecular cloning of HEK, the gene encoding a receptor tyrosic kinase expressed by human lymphoid tumor cell lines proc. Natl. Acad. Sci. U.S.A. 89 (5), 1611-1615 (1992)
                                                                                                                                                                                                Human receptor tyro
M83941
M83941.1 GI:183931
                                                                                      Proc. Natl. Acad. 92179233
                                                                                                                                                                    Homo sapiens
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Homo sapiens lymphoid tumor cDNA
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receptor tyr
               /organism="Homo sapiens"
/db_xref="taxon:9606"
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/tissue_type="lymphoid tumor"
101. 3052
/gene="
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Query Match Best Local S Matches 813

Local Similarity 100 nes 813; Conservative

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Score 813; DB 9; Pred. No. 4.3e-241; ; Mismatches 0;

Length Indels

3149; 0

Gaps

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101 61

gaactgattccgcagccttccaatgaagtcaatctactggattcaaaacaattcaaggg

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gagctgggctggatctcttatccatcacatgggtgggaagagatcagtggtgtggatgaa

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aacctgtactacatggagtctgatgatgatcatggggtgaaatttcgagagcatcagttt TTCACTCTACGAGACTGCAATAGCATTCCATTGGTTTTAGGAACTTGCAAGGAGACATTC ttcactctacgagactgcaatagcattccattggttttaggaacttgcaaggagacattc

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ttggcatttcaagatgttggtgcttgtgttgccttggtgtctgtgagagtatacttcaaa

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ISYPSHGWEELSGVDEHYTPIRTYQVCNYMDHSQNINKLERIWYPERNSAQKIYVELKET
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MLCWOXDRINNRPKFEQIVSILDKLIRAPGSLKIITSAAARPSNLLLDQSNVDISTFR
TTGDWLMGVFTAHCKEIFTGVEYSSCDTIAKISTDDMKKVGVTVVGPQKKIISSIKAL
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/codon_start=1
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/protein_id="AAA58633.1"
/db_xref="GI:183932"
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Rattus norvegicus eph-related
(Rek4) mRNA, complete cds.
U69278 U69278.1 GI:1943913
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L1,Y.Y., McTlernan,C.F. and Feldman,A.M.
Direct Submission
Submitted (01-SEP-1996) Cardiology, University of Pittsbur Lothrop Street, Pittsburgh, PA 15213, USA
On Apr 18, 1997 this sequence version replaced gi:1698721.
Location/Qualifiers
1. 3077
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Eutheria; Rodentia; Sciurognathi; Muridae; Murid
1 (bases 1 to 3077)
Li,Y.Y., McTiernan,C.F. and Feldman,A.M.
II-1 beta alters the expression of the receptor
gene r-EphA3 in neonatal rat cardiomyocytes
and J. Physiol. 274 (1), H331-H341 (1998)
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    877
                                                       /product-"peh-related receptor tyrosine kinase homolog"
/db_xref="GI:1698722"
/db_xref="GI:1698722"
/translation="MMCHLSILILIEGCCVLSCSRELSPQPSNEVNLLDSKTIQGELGW
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ILKLWTEIREYGPVNKKGFTLAFQDVGACVALVSYRYFKKCPFTVKNLLAMEPDTVPM
DSQSLVEVRGSCVNNSKEEDPPRNYCSTEGEWLVPIGKCTCNAGYEERGFICQACRPG
FYKALDGVAKCTKCPPHSSTQEDGSMNCRCENTYFABXDPPSNAGTRAPSAPRNVIS
INNTSYLLDWSWPLDTGGRGITTNUCKKCGWNYFABXDPPSNAGTRAPSAPRNVIS
NINTSYLLDWSWPLDTGGRGITHNICKKCGWNYFABXDPPSNAGTRAPSAPRNVIS
NINTSYLLDWSWPLDTGGRGITLDYSYKYEKCDGTSYTILAARGTNVTISSLKPDTTYVFQ
IRAFTAAGYGTNSKKEEFENSPDSFSISGENSHVWMIAISAAVAIIVLTVTVTYLVGR
FGCYIKSKHSSDERKLHFGNGHLRLPGLRTYVDPHTXDDFDQAVHEFAKELDANNIAI
DKYVGAGEFGBVCSGRLKLPSKKEISVAIKTLKVGYTEKQRRDFLGEASIMGGFDHPN
IIRLEGYVTKSKPVMIVTEYMENGSLDSFLKHDAGFTVIGLVGMLRGTASGMKYLS
MGYVHRDLAARNILINSNLVCKVSDFGLSRVLEDDPEBAYTTRGCKILPWMTSPEATA
YRKFTSASDVMSYGIVLMEVMSYGERPYWEMSNQDVIKAVDEGYRLPLPMDCPAALYQ
LMLDCWGKDRNNRFKFEGIVSILSKLINGSKLSITTSAAARPSNLLLDGSNVDIATF
HTTGNATINGMFFAHCKEFTFTGVEYSSCOTTIAFTSTDMWKXVCVTVVCGDXKITSGTKA
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35. .2989
                                           HTTGDWLNGMRTAHCKEIFTGVEYSSCDTIAKISTDDMKKVGVTVVGPQKKIISSIKA
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/dev_stage="neonatal"
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Sciurognathi; Muridae; Murinae;
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ACCESSION VERSION KEYWORDS SOURCE

m68515 M68515.1 MUSMEK4SE Mouse eph-

receptor tyrosine kinase. Mus musculus (strain IRC

×

Swiss Webster) 11.5

day embryo embryo

GI:454828

RESULT 5
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LOCUS

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DEFINITION

k4SE 2032 eph-related cas.

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(Mek4)

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                                                                              cagtccctggtggaggttagagggtcttgtgtcaacaattctaaggaggaagatcctcca
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GCTGGGTATGAAGAACGAGGGTTCATATGCCAA
                                                                      CAGTCCTTGGTGGAGGTTAGGGGCTCTTGTGTCAATAATTCCAAGGAGGAGGACCCTCCC
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                                                                                                        AAGTGCCCATTTACAGTGAAGAATCTGGCTATGTTTCCAGACACAGTGCCCATGGACTCC
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Pred. No. 2e-1
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TITLE
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Best Local Similarity
Matches 725; Conserv
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acaaagattgacaccattgcagctgatgaaagtttcactcaaatggatcttggggaccgt 480
                                                                                          TTCACACTGCGGGACTGTAACAGCATTCCATTGGTTTTTGGGGACTTGCAAGGAGACCTTT
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Sajjadi,F.G., Pasquale,E.B. and Subramani,S. Identification of a new eph-related receptor tyrosine kinase from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor New Biol. 3, 769-778 (1991)
                                                                                                                                                        On Feb
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lrdcnsiplylafotckeffnlyymesddhgvkfrehoffnthodri
lklntelrevgevnkkoeylafodhgvkfrehoffnthodri
lklntelrevgevnkkoeylafodvgavoyalvsvryyfkkoeptryknlamfpdtypmd
soslvevrgscvnnskeedpprnycstegewlvpigkcfonagysergficqacregf
ykasdcarkcakcphhsstoedosmncrennyfraekdppsmacarppsaprnvisn
inetsvildmsmplotogrkdiffnickkoemvrqcepcspnvrflproligittt
vtvddllahtnyffeidavngvselsspprqyaavsjtmvapspymiikkdrysrn
sislsmoepehbngiildyevktygkoboetsytilrargtnytisslkpdttyvfqi
rartaagygtnsrkfefetspdcmyyfsf"
2010. 2015
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/protein_id="AAA39522.1"
/db_xref="GI:454829"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/Strain="IRC x Swiss Webster"
/db xref="taxon:1090"
/dev_stage="11.5 day embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , 1994 this sequence version Cocation/Qualifiers
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89.2%;
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Identification of a new eph-related receptor tyrosine from mouse and chicken that is developmentally regulat encodes at least two forms of the receptor New Biol. 3, 769-778 (1991)
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/Codon_start=1
//Codon_start=1
//protein_id="receptor tyrosine kinase"
//protein_id="AAA39521.1"
//db_xref="GI:199120"
//db_xref="GI:199120"
//translation="MDCHLSILVLLGGCVLSCSGELSPOPSNEVNLLDSKTIQGELGW
//translation="MDCHLSILVLLGGCVLSCSGELSPOPSNEVNLLDSKTIQGELGW
//translation="MDCHLSILVLLGGCVLSCSGELSPOPSNEVPRNSAQKIYVEKET
LRCNSIPLVLGTCKEFFNLYKMESDDHGVKFTEHQFTKNDTIAADESFTQMDLGDRI
LKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRTVFKKCPTVKNLAMFPDTVPMD
SOSLVEVRGSCVNNSKEEDPPRMYCSTEGEMLVPIGKCTCNAGYEERGFICQACRPGF
YKASDGAAKCAKCPHSSTQEDGSMNCRCENNYFRAEKDPPSMACARPPSAPRNYISN
INETSVILMSWPLDTGGRKDITFNIICKKCGMNVRQCEPGSBNVRFLPRQLGLTNTT
VTVTDLLAHTNYTFEIDAVNGVSELSSPPRQYAAVSITINQAAPSPVMTIKKDRTSRN
SISLSNGDEBENGIILDYEWKYYQKOEQETSYTILKARGTNYTISSLKPDTTYVFQI
RARTAAGGYGTNSRKFEFETSPDSFSISGENSHVVMIAISAAVAIIVLTVVTYVLVGRF
                                                                                                                                                                                                                                                                      /gene="Mek4"
89. .3040
                                                                                                                                                                                                                                                                                                           /tissue_type="embryo"
89. .3040
                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus"
/strain="IRC x Swiss Webster"
/db_xref="taxon:10090"
/dev_stage="11.5 day embryo"
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ATCTCCTACCCATCACATGGGTGGGAAGAGATTAGTGGTGTTGATGAGCATTATACTCCA
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On Feb 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identification of a new eph-related receptor tyrosine kinase from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor New Biol. 3, 769-778 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aves: Neognathae; Gallitormes; rnasiauluae, 1 (bases 1 to 3241)
1 (bases 1 to 3241)
Sajjadi,F.G., Pasquale,E.B. and Subramani,S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gallus gallus 10 day embryo
Gallus gallus
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Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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sypshgweeisggvdehytpirtygesgrumdhsonnwlrtnwiprnsagriyvelketl
RDCNSIplvlgcketfniyymesdddhilakrerdfrindiaadesftomdlegdri
LKLNTEVREVeptykKREftlargdvgacvalvsyryfekkCpftyknlawfepgriydmd
SQSLVEVRGSCVNHSKEEEPPKMYCSTEGEWLVPIGKCLCNAGYEERGFACOACRPGF
YKASAGNYKCAKCPHSSTYEDASLNCRCEKNYFRSEKDPSMACTRPBSAPRNVISN
INETSVILDWSWPLDTGGKRUYTFNIICKKCGGSSKICEPCSDNVRFLPROTGLINTT
VTVVDLLAHTNYTFEIDAVNGVSDLSTLSRQFAAVSITTNQAAPSTITVIRDRTSKN
SVSLSWQEPEHPNGIILDYEYKYYEKCEOEXTYTLRAKSTNVTISGLKPDTTYVFQI
RARTAARYGTSSKFEFETSPDSFSISSNSQVVMIAISAAVAIILLTVVVYVLIGRE
CGYKKSKHGTDEKRLHFGGHLKLPGLGTYDDHTYEDDNOAVHEFAKELDASNISID
KVVGAGEFGEVCSGRLKLPSKKEISVAIKTLKAGYTEKQRRDFLGEASIMGOFDHPNI
IRLEGYVTKSKRYMIVTEYMENGSLDSFLRKHDAQFTVLOLVGMLRGIASGMKYLSDM
GYVHRDLAARNILINGNLYCKYSDFGLSRTLEDDPSAAYTTRGKKIPIRTSPEAIAY
RKFTSASDAWSYGIVLWEVMSYGERPYWEMSFQDVIKAVDEGYRLDPDMCCPAALYQL
MKDCHOKORNNRAFKFEDIVSILDKLINDRSCKIITINAAPSNILLDGSNIDISAFR
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/codon_start=1
/codon_start=1
/product="receptor tyrosine
/protein_id="AAA48666.1"
/db_xref="GI:211447"
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/db_xref="taxon:9031"
/dev_stage-"10 day embryo"
/tissue_type="embryo"
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GAGAGAGGCTTTGCGTGCCAA 841
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Sequence
115007
115007.1
                                                                                                                                                                  Unknown.
                                                                                                                             Unclassified.

1 (bases 1 to 3254)

Pasquale, E.B. and Sajjadi, F.G.

Eph-related tyrosine kinases, nucleotide
                                                                                                                Patent:
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                           Conservative
                                                                          US 5457048-A 15 10-OCT-1995;
Location/Qualifiers
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/organism="unknown"
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0; Mismatches 160;
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      Ohta,K., Nakamura,M., narvana...
Ando,M. and Tanaka,H.
The receptor tyrosine kinase, Cek8, is transiently expressed
The receptor tyrosine kinase, Tek8, is transiently expressed
                                                                        D38174.1 GI:1236732
receptor tyrosine kinase;
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Gallus gallus
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subtypes of motoneurons in Mech. Dev. 54 (1), 59-69 (1 96404128
                                                         Eukaryota; Metazoa; Chordata; Aves; Neognathae; Galliformes;
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                                                         Craniata; Vertebrata; Arch; Phasianidae; Phasianidae;
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                                                  gtccccaggaactcagctcagaagatttatgtggagctcaagttcactctacgagactgc
                                                                                  acttaccaggtgtgcaatgtcatggaccacagtcaaaaacaattggctgagaacaaactgg
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                                    ATTCCCCGCGAGGGGCTCAGAGGGTATATATTGAAATCAAGTTCACGCTGAGAGACTGC
                                                                                                                                 CCGCTGGAAGGAGGGAGGAAGTGAGCATAATGGATGAGAAGAACACTCCGATCCGC
                                                                                                                                                                               AACGAAGTGACCCTGCTGGACTCCCGCTCGGTGCAGGGGGGAGCTGGGCTGGATCGCGAGC
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Direct Submission

Submitted (09-SEP-1994) to the DDBJ/EMBL/GenBank databases.

Kunimasa Ohta, Kumamoto University Graduate School of Medical Sciences, Dept. of Neuroscience and Immunology; 4-24-1 Kuhonji, Kumamoto, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
3 (bases 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue_type="spinal cord"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Gallus gallus"
/db_xref="taxon:9031"
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                                                                                                                                                                                                                                                    Direct Submission
Submitted (14-MAY-1996) Pathology & Laboratory Medicine, I
Submission Malk, Philadelphia, PA
                                                                                                                                                                                                                                                                                                                                                   Lee,A.M., Navaratnam,D., Ichimiya,S., Greene,M.I. and Davis,J.G. Cloning of m-ehk2 from the murine inner ear, an eph family receptyrosine kinase expressed in the developing and adult cochlea DNA Cell Biol. 15 (10), 817-825 (1996)
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U58332.1 GI:1457960
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3943)
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                                                                                                                                                    /organism="Mus musculus"
/strain="Balb/c"
/db_xref="taxon:10090"
285. .3392
/product="receptor tyrosine kinase"
/protein_id="AAB53836.1"
/db_xref="G1:1457961"
/translation="MGGCEVREFILOFGFFLPLLTAWTGDCSHVSNQVVLLDTTTVMG
ELGWKTYPLNGWDAITEMDEHNRPIHTYQVCNVMEPNQNNWLRTNWISRDAAQKIYVE
                                                                                                /note="eph-related tyrosine kinase; similar norvegicus receptor-like tyrosine kinase Ehl Accession Number S51605"
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GCTGATGGGGATTGGCTTGTTCCTCTTGGAAGGTGTATCTGCAGTACAGGGTATGAAGAA
                                         acagaaggcgaatggcttgtacccattggcaagtgttcctgcaatgctggctatgaagaa 795
                                                                                                                                                                                                         GGAGCATGCATCGCTCTGGTCTCAGTCCGAGTTTTCTACAAAAAATGCCCCTTCACCGTG
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LGDRILKLNTEIREVGEIERKGFYLAFQDIGACIALVSYNFYEKKCPFFVRSLAMFPD
TIPRVDSSLYEVRGSCVKSAEEDDTFKLYCGADGDMLVPLGRCICSTGYEEIEGSCH
ACRPGFYKAFAGNTKCSKCPPHSSTYVEATSVCHCEKGYFRAEKDPENMACTRPPSAP
RNVAFNINETALILEMSPPSDTGGRKDLTYSVICKKCGLDTTQCEDCGGGLRFIPRHT
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X78689
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1 (bases 1 to 3531)

Taylor, V., Miescher, G.C., Pfarr, S., Honegger, P., Breitschopf, Lassmann, H. and Steck, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Maisonpierre, P.C., Barrezueta, N.X. and Yancopoulos, G.D. Ehk-1 and Ehk-2: two novel members of the Eph receptor-like tyrosine kinase family with distinctive structures and neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (07-APR-1994) G.C. Miescher, Neurological Clinic & Research Dept., University Hospitals Basel, 4031 Basel, SWITZERLAND
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THEEASTSCVCEKDYFRRESDPPTMACTTPSPVTNVKKKIAKNSISLSWQEDDPNNG
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publ. seq. and PCR cDNA fragments)"
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/replace="g"
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APEALAPRKFTSASDVWSYGIVMWEVVSYGERPYWEMTWODVIKAVEEGYRLPSPMDC
PAALYQLMLDCWQKDRNSRPKFDDIVNMLDKLIRNPSSLKTLVNASSRVSTLLAEHGS
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Maisompterre, P.C., Masiakowski, P. and
Ehk and Ror tyrosine kinases
Patent: US 5843749-A 102 01-DEC-1998;
Location/Qualifiers
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Caras, I.W. and Winslow, J.W.
AL-1 neurotrophic factor antibodies
Patent: US 5798448-A 1 25-AUG-1998;
Location/Qualifiers
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Gilardi-Hebenstreit, P., Nieto, M.A., Frain, M., Chestier, A., Wilkinson, D.G. and Charnay, P. An Eph-related receptor protein tyrosine kina
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Submitted (26-MAR-1992)
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                                                                                                                        Eukaryota; Metazoa;
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            expressed in the developing mouse hindbrain Oncogene 7 (12), 2499-2506 (1992) 93096484
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/note="Eph receptor related
/note="Eph receptor related
/codon_start=1
/product="tyrosine kinase"
/protein_id="CAR46268.1"
/db_xref="MGD:MGI:98277"
/db_xref="MGD:MGI:98277"
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58. .3018
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LKTTRYSITDLLAHTNYTFELWAVNGYSKYNESPDQSYSVTVTNQAAPSSIALVQAK
EVTRYSVALAGUEPDRENGVILEYEVKYYEKDADSYSVTVTNQAAPSSIALVQAK
EVTRYSVALAGUEDESEPLEVTTNYVPSRIIGDGANGTVLLVSVSGSVVLVVILLA
YVISRRRSKYSKAKQEADEEKHLNQGVRTYVDFTYEDPNQAVREFAKEIDASCIKIE
KYIGVGEFGEVCSGRLKYPGKREICVALKTLKAGYTDKQRDFLSEASIMGQDHPNI
IHLEGVTKCKFVMIITEYMENGSLDAFLKKNDGRFTVIQLVGMLRGIGSGMKFLSDM
SYVHRDLAARNILVNSNLVCKYSDFGMSRVLEDDPEAAYTTRGGKIFIRMTADEAIA
KTITSASDVWSYGIVMMEVMSYGERPYWDMSNQDVIKAIEEGYRLPPPMDCFIALHQL
RLDCHQGKERSDRYKFGGIVNMLDKLIRNPNSLKRTGSBSSRFNTALLDPSSPEESAVV
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FTLRDCNSLPGVMGTCKETFNLYYYESDNDKERFIRESQFGKTDTIAADESFTQVDIG
BRIMKLWTEIRDVGPLSKKGFYLAFQDVGACIALVSVRVFYKKCCLTVRNLAQFFDTI
TGADTSSLVEVRGSCVMNSEEKDVFKMYCGADGEWLVPIGNCLCANGHEERQNBECOG
KIGYYKALSTDASCAKCPPHSYSVWEGATSCTCDRGFFRADNDAASMPCTRPPSAPLN
                                                                                                                                                                                                                                                                                                                                          /gene="Sek"
/product="tyrosine kinase"
/2392. .2394
/gene="Sek"
/gene="Tyrosine autophosphorylated"
/note="tyrosine autophosphorylated"
1034 c 1052 g 1001 t
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103. .3015
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/db_xref="taxon:10090"
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Mus sp.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;

Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

1 (bases 1 to 4242)

1 (bases 1 to 4242)

1 (bases 1 to 4242)

1 (bases 1 to 4242)
                                                                                                                                                                           GenBank staff at the National Library of Medicine created this entry (NCBI gibbsq 127779) from the original journal article. This sequence comes from Fig. 5.
*ERRATUM* Gilard: Hebenstreit et al., Oncogene (1992)7, 2499-2:
                                                                                                                                                                                                                                                                                                            Gilardi-Hebenstreit, P., Nieto, M.A., Frain, M., MB Chestler, A., Wilkinson, D.G. and Charnay, P. An Eph-related receptor protein tyrosine kinase expressed in the developing mouse hindbrain oncogene 8 (4), 1103 (1993)
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                  /note="Eph-related receptor protein tyrosine kinase" 58. 3018
                                                                                                       /organisma"Mus sp."
/db_xref="taxon:10095"
/gene="Sek"
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                                               GATGTGGGTGCTTGCATCGCCCTGGTGTCTGTCCGTGTGTTCTACAAGAAGTGTCCACTC
                                                                                 aacactgagattagagaagtaggtcctgtcaacaagaagggattttattttggcatttcaa
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WIASPLEGGWEEVSIMDEKNTPIRTYQYCNVMEASQNWRLRTDWITREGAQRVIEIK
FTLRDCNSLPGVMGTCKETFNLYYYESDNDKERFIRESOFGKTDTIAADESFTQVDIG
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TGADTSSLVEDRGSCVNNSEEKDVPKWYCGADGEWLVPIGNCLCNAGHEEQNGECQAC
KIGYYKALSTDASCAKCPPHSYSVWEGATSGTCCRGFFRADNDAASMFCTRPPSAPLN
LISNUNETSVHLEWSSPQNTGGRQDISVNVCKKGGADDPSKCRECGGGVHTPOQNK
LKTTRVSITDLLAHTNYTFEIWAVNGVSKYNPSPDQSVSVTVTTNQAAPSSIALVQAK
EVTRYSVALAWLEPDRENGVILLYEVKYYEKDONERSYRIVRTAARNTDLKGLAPLIS
YVFHVRARTAAGYGDFSEPLEVTINTVPSRIIGDGRANSTVLLVSVSGSVVLVVILIAA
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RKFTSASDVWSYGIVMMLDKLIRWFSKSVDDVIKAIEEGYRLPPMDCPIALHQL
MSYVHRDLAARNILVKYSDFGMSRVLEDDPEAAYTTRGKGIPIRWFDFBAIAY
RKFTSASDVWSYGIVMMLDKLIRWFNSLKTTGSSSRPNTALLDPSSPEFSAVV
SYGDWLQAIKWRYKINFTAAGYTTLEAVVHMSQDDLARIGITAITHQNKILSSVQAM
RTQMQQMHGRWVPV*

1034 c 1052 g 1001 t
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*ERRATUM* Gilardi-Hebenstreit et al., Oncogene (1992) 7,
2499-2507; This sequence comes from Fig. 5*
/codon_start=1
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Pred. No. 6.7e-98;
0; Mismatches 263;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammal: Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 435)
Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucabb,T., Le,M., Lennon,G., Marra,! Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.

The WashU-Merck EST Project
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AV044999 AV044999
AV393461 AV393461
AW239735 U657c05.y
AV153845 AV153845
AF116297 Armillari
AA952881 On76f10.s
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AA952881 CN76f10.s
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AQ910535 GSSTc0577
R37827 yh97e67.s1
AA825079 L30-102T3
AA709190 a120e09.s
A1187362 gf29b07.x
AA426374 zv54h01.s
AA426374 zv54h01.s
AA426377 RPCI-23-3.s
AQ920797 RPCI-23-3.s
AQ920797 RPCI-33-3.s
AQ920797 RPCI-33-3
AW266010 L30-2671T
A122984 L30-2671T
A1208021 gg60g06.x
A1205604 gg30f11.x
A131975 fa95h11.y
A1331975 fa95h11.y
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AA865380 oh49f01.s
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AQ850374 LMAJFV1_1
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Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Lourel: 314 286 1800
Fax: 314 286 1810
Email: estewatson.wustl.edu
Insert Size: 2663
High quality sequence stops: 276
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Eutheria; Primates; Catarrhini; Hominidae; Ho
1 (bases 1 to 427)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="GDB:3847311"
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/clone_1ib="Soares retina N2b4HR"
/clone_1ib="Soares retina N2b4HR"
/sex="male"
/dev_stage="55 year old"
/note="forgan: eye; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Ist strand cDNA was primed with Not I; Site_2: Eco RI; Ist strand cDNA was size selected, ligated to Eco RI sites of a modified pT7T3 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(A)+ RNA was extracted 6 hrs after their removal. The retina RNA was extracted 6 hrs after their removal. The retina RNA was extracted 6 hrs after their removal. The retina RNA was shadly provided by Roderick R. McInnes M.D. Ph.D. from the University of Toronto. Library constructed by Bento Soares and M.Fatima Bonaldo. " 6 others
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                            427 bp mRNA EST 12-MAR-1998 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1469977 3' gb:M17887 60S ACIDIC RIBOSOMAL PROTEIN P2 (HUMAN);, m
                                                                                             Chordata; Craniata; Vertebrata; Catarrhini; Hominidae; Homo.
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Large-scale Sequencing Analysis of Unpublished (1998)
On May 8, 1995 this sequence vers. Contact: Eun M.Y.
Department of Cytogenetics
National Inst. of Agri. Sci. and Suwon, Kyunggido, Korea
                                                                                                                                                                                                                                                                                                                                                                          cDNA clos
AA752361
                                                                                                                                             1 (bases 1 to 225)
Nahm,B.H., Kim,J.K., Cheong,J.J., Kim,S.I., Hahn,T.R, Moon,E.P.,
Kim,W.T., Kim,W.Y., Yang,M.S., Park,R.D., Sohn,U.I., Kang,K.Y.,
Lee,M.C. and Eun,M.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                AA752361
96GS0872 Rice
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On Jan 14, 1998 this sequence version replaced gi:1798438
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnollophyta; Liliopsida; Poales;
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                                                                                                                                                                                                                                                                                        Oryza sativa
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h quality sequence stop: 373.
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0872 Rice Immature Seed Lambda
clone 96GS0872, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1469977"
/clone_lib="NCI_CGAP_GC4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host="DH10B"
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                     and Tech,
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Library construction: Natalia S. Akopyants, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
If using this information please cite:
N.S. Akopyants and S.M. Beverley 'A survey of the Leishmania major
Friedlin strain V1 genome by shotgun sequencing' and the Washington
University Genome Sequencing Center For information on obtaining
                                                                                                                                                                                                                                                                                     Unpublished (1999)
On Mar 23, 1999 this sequence version
Other_GSSs: lm30b08.x1
                                                                                                                                                                                                                                                                                                                                                                                      Akopyants, N.S., Beverley, S.M., Clifton, S., Marra, M., Hillier, L., Chinwalla, A., Pape, D., Martin, J., Wylie, T., Blistain, A., Schmitt, A., Person, B., Theisin, R., Ritter, E., Ronko, T., Schmitt, A., Cole, R., Underwood, K., Cardenas, M., Gibbons, M., Harvey, N., McCann, R., Tsagareishvili, R., Williams, T., Jackson, Y., Bowers, Y., Swaller, T., Waterston, R. and Wilson, R.
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Submitted by Baek Hie Nahm, Dept of Biological Science, Myongji
University, Yongin, Korea. 449-728 bhnahm@bioserver.myongji.ac.kr
Seq primer: M13 Reverse Primer.
                                                                                                                                                                                                           Contact: Akopyants, NS / Beverley, SM WashU Leishmania Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                   WashU Leishmania Project
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                                                                                                                                            Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Rice Immature Seed Lambda ZAPII cDNA Library"
/tissue_type="Immature Seed"
/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Oryza sativa"
/cultivar="Milyang23"
/db_xref="taxon:4530"
/clone="96GS0872"
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Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Pred. No. 77;
0; Mismatches
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AU033295/c
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                                                                                                                                                                                                                                                                                                  Unpublished (1997)
On Jan 17, 1998 this sequence version replaced
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program
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AU033295
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Seq primer: -40RP from Gibco
Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                       Yamamoto, K. and Sasaki, T. Yamamoto, K. and Sasaki, T. Rice cDNa from etiolated shoot Unpublished [1997]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oryza sativa.
Oryza sativa
                                                                                                                                                                                                        Tel: 0298-38-7441
Fax: 0298-38-7468
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euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
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Location/Qualifiers
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                                                                                                                                                                   tsasaki@abr.affrc.go.jp
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/lab_host="ToP10 (Invitrogen)"
/note="Vector: p2ero-2 (Invitrogen); Site_1: EcoRV;
Genomic DNA was isolated from stationary phase cells. For
this library, DNA was sheared to give a tight size
distribution of 1-1.5kb fragments, blunt-ended with T4 DNA
polymerase, dephosphorylated with Shrimp Alkaline
Phosphatase and ligated into p2ero-2 vector's EcoRV site."
a 148 c 107 g 90 t
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/organism="Oryza sativa"
/strain="Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
/clone="86421_la"
/clone_lib="Rice shoot"
/note="Etiolated shoot (8 days old)"
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/strain="Friedlin strain V1"
/db_xref="taxon:5664"
/clone="LMAJFV1_lm30408"
                                                                                                                                              Location/Qualifiers
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Matches 48; Conserv
Query Match
Best Local Similarity
Matches 43; Conserv
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Unpublished (1999)
On Jun 5, 1998 this s
Contact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K., Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T., Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M., Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Niitsuma,H., Oda,J. Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Tateno,M., Tomaru,Y., Tominaga,N., Watanabe,S., Yagame,M., Yamamura,T., Yokota,T., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermosciivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
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Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 322)
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/clone="1700040E03"
                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/strain="C57BL/6J"
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/sex="male"
                                                                                                                                                                                    /dev_stage="adult"
96 c 62 g
                                                                                                                                                                                                                                              /tissue_type="testis"
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                         32.2%;
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Pred. No. 1.3e+02
0; Mismatches 3:
Score 28; DB 50;
Pred. No. 1.4e+02;
0; Mismatches 25
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1 (bases 1 to
             Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 518)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Pro
                                                                                                                                                                                                                                AW230735 518 bp mRNA EST 10-DEC-1999 uc67c05.yl NCI_CGAP_Maml Mus musculus cDNA clone IMAGE:2647592 5' similar to gb:D21089 DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS (HUMAN); mRNA sequence.

AW230735 AW230735.1 GI:6560031
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AV393461 GI:6547677
                                                                                                                                                                                                           EST
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Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
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Gene Index
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/clone=1lb="Chlamydomonas reinhardtii C9"
/dev_stage="photoautotrophic growth"
/note="Vector: pBluescriptII SK-; Site_1:
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/strain="C9"
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22 ctcctccttctcagctgctctgttctcgacagcttcggggaactgattccgcagccttcc 81
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1 (bases 1 to
                                                                                                                                                                                                      Unpublished (1999)
On May 18, 1998 th
Contact: Chie Owa
3-1-1 Koyadai, Tsukuba,
Tel: 81-298-36-9145
Fax: 81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AV153845 Mus muscullus hippocampus C57BL/6J
clone 2900058C14, mRNA sequence.
AV153845
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Tissue Procurement: Glibert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing C
Clone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1997)
On Jul 9, 1999 this sequence version replaced g1:5434208.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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Eutheria; Rodentia;
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site_2: NotI; Cloned unidirectionally. Primer: Oligo dr
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
a 116 c 163 g 68 t 2 others
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/dev_stage="3 months, virgin"
/lab_host="DH10B"
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/clone="IMAGE:2647592"
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/strain="FVB/N"
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66.7%;
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Pred. No. 1.7e+02;
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Submitted (23-DEC-1998) Biology, University of Toronto at
Submitted (33-DEC-1998) Biology, University of Toronto at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AF116297 291 bp Dr
Armillaria gallica strain
AF116297
                                                                                                                                                                                                                                                                                                                                                                                                         Armillaria gallica.
Armillaria gallica
Eukaryota; Fungi; Basidiomycota;
Tricholomataceae; Armillaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                     2 (bases 1 to 291)
Anderson, J.B. and Hodnett, B.
                                                                                                                                                                                                                                                                                                                                   Michigan hardwood forest
Unpublished
                                                                                                                                                                                                                                                                                                                                                                Random nuclear DNA sequences of Armillaria
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                                                                                                                                                                                                                               Location/Qualifiers
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="2900058C14"
                                                                                                                                                     /db_xref="taxon:47427"
94 c 72 g
                                                                                                                                                                                /organism="Armillaria gallica"
/strain="C33r"
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75 c 80 g
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Pred. No. 1.8e+02;
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1.6e+02;
hes 22;
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AA282730 402 bp mRNA EST 13-AUG-1997 zs89h08.rl NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:704703 similar to TR:G1049078 G1049078 SRP30C. ;, mRNA sequence. AA282730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
On Jan 17, 1998 this sequence version replaced Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA952881 329 bp mRNA EST on76f10.sl Soares_NFL_T_GBC_S1 Homo sapiens IMAGE:1562635 3', mRNA sequence.
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                                                                                                                                                                                                 77
                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and s circles were made in vitro: Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                             Soares and M. Fatima Bonaldo.
1 102 c 82 g 68 t
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/clone_lib="Soares_NFL_T_GBC_S1"
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/db_xref="taxon:9606"
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                                                                                                                                              247
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Pred. No. 1.9e
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nes 29;
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AI869632
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w199d07.x1 NCI_CGAP_Brn25 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1997)
On May 8, 1995 this sequence version replaced gi:800900.
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 419)
NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
                                                                        Homo sapiens
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1 (bases 1 to 402)
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EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: Robert_Strausberg@nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3/]. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not RI sites of the modified pT/73 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo."

82 c 108 g 110 t
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/db_xref="taxon:9606"
/clone="IMAGE:704703"
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/lab_host="DH10B"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 484)

NCI/NINDS-CGAP http://www.ncbi.nim.nih.gov/ncicgap.

National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index
Unpublished (1998)

On Dec 20, 1995 this sequence version replaced gi:1133839.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1998)
On Jun 22, 1998 this sequence version Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                  AI992021 484 bp mRNA EST W$44b02.x1 NCI_CGAP_Brn25 Homo sapiens cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: (301) 496-1550
                                                                                                                                                                                                                                                                  mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library is normalized, and was constructed by Bento Soares and M.Fatima Bonaldo."

131 c 104 g 88 t
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Fugu rubripes

Fugu 
                                                                                                                                                           Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource Centre Hinxton, Cambridge, CB10 1SB. Email: biohelpehgmp.mrc.ac.uk Vector: pBluescript II KS
                                                                                                                                                                                                                                                                                 Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrania,Y.,
Williams,G. and Brenner,S.
Direct Submission
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AL012136.1 GI:2677569
GSS; genome survey sequ
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-GGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
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Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,
sequence
                                                                                                                                    V_type: phagemid
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                         pass dye-terminator sequencing of cosmid cloned genomic
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/lab_host="DH10B"
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Pred. No. 2.1e+02;
0; Mismatches 29;
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COMMENT

TITLE

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BASE COUNT
ORIGIN
                                                                                          FEATURES
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a 131 c 98 g 140 t
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            11
            others
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                                                              Query Match
Best Local :
                                                  Matches
                                                Local Similarity 67.2
mes 39; Conservative
  82
             9 tcagctctccatccttcttctcagctgctctgttctcgacagcttcggggaactg
TCAGCTGTGCTTCCTCCACCTTCAGCAGTGCTGGGTTTTTTGCCTGCTTACGGGTCCTG
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                                                : Score 27.6; DB
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0; Mismatches
                                                           27.6; DB 82
No. 2.2e+02;
                                                 Indels
                                                                        Length 549;
                                                 0
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Search completed: May Job time: 19138 sec 15, 2000, 11:20:15

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Database :
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Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
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Perfect score:
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length: 1000000
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87
1 atggattgtcaqct
            Pending_Patents_NA:*
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cgn2_6/ptodata/2/pna/US09B_COMB.seq:
cgn2_6/ptodata/2
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result		Query				
No.	Score	Match	Match Length DB ID	B		Description
ب	87	100.0	87	40		Sequence 6, Appli
2	87	100.0	813	40	40 US-09-104-340-5	Sequence 5, Appli
α ω	31	35.6	453	92	92 US-60-172-375-1200	Sequence 1200, Ap

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LENGTH: 87
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CORGANISM: Homo sapiens
FEATURE:
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LOCATION: (1)..(87)
OTHER INFORMATION: Exon I
US-09-104-340-6
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GENERAL INFORMATION:
APPLICANT: BOYD, Andrew W
APPLICANT: BOYD, Andrew W
APPLICANT: LACKMANN, MAITIN
TITLE OF INVENTION: RECEPTOR-LIGAND SYSTEM AND ASSAY
FILE REFERENCE: boydug
CURRENT APPLICATION NUMBER: US/09/104,340
CURRENT FILING DATE: 1998-06-25
EARLIER FILING DATE: 1997-06-25
NUMBER OF SEG ID NOS: 25
NUMBER OF SEG ID NOS: 25
SOFTWARE: Patentin Ver. 2.0
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US-09-104-340-6
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0 US-60-133-875-1293
0 US-60-133-875-1443
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Sequence 1243, Ap
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Sequence 2003, Ap
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US-09-104-340-5
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(Sequence 5, Application US/09104340
(SENERAL INFORMATION:
APPLICANT: BOYD, Andrew W
APPLICANT: DOTORI, MITCELLA
(APPLICANT: LACKMANN, MARTLIA
(APPLICANT: LACKMANN, MARTLIA
(CURENT APPLICATION: RECEPTOR-LIGAND SYSTEM AND ASS)
(FILE REFERENCE: boydug
(CURRENT FILLING DATE: 1998-08-25
(CURRENT FILLING DATE: 1998-08-25
(EARLIER APPLICATION NUMBER: P07549
(EARLIER APPLICATION NUMBER: P07549
(EARLIER FILLING DATE: 1997-06-25
(NUMBER OF SEQ ID NOS: 25
(SOFTWARE: Patentin Ver. 2.0
(SEQ ID NO 5
(SEQ ID NO 5
(CURRENT)
(CORGANISM: Homo sapiens
                                                                         RESULT 3
US-60-172-375-1200/c
US-60-172-375-1200/c
Sequence 1200, Application US/60172375
GENERAL INFORMATION:
APPLICANT: Schuch, Wolfgang
APPLICANT: Code, Martin
APPLICANT: O'Neill, John M.
APPLICANT: O'Neill, John M.
FILE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM WHEAT CARYOPSIS
FILE REFERENCE: PL-0051 P
CURRENT APPLICATION NUMBER: US/60/172,375
CURRENT APPLICATION NUMBER: US/60/172,375
UNMBER OF SEQ ID NO:: 11151
SOFTWARE: PERL Program
SEQ ID NO 1200
LENGTH: 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; FEATURE:
NAME/KEY: exon
LOCATION: (1)..(813)
OTHER INFORMATION: Exons I,
US-09-104-340-5
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Best Local Similarity 100.0%;
Matches 87; Conservative 0;
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Best Local Similarity
Matches 87; Conserv
                                TYPE: DNA ORGANISM: Triticum aestivum FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Inc
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No. 2.7e-16;
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US-60-185-359-1293 Application US/60185359

Sequence 1293, Application US/60185359

GENERAL INFORMATION:

APPLICANT: Venter, J. Craig

TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic

TITLE OF INVENTION: Acid Sequences, Systems Containing The Nucleic Acid

TITLE OF INVENTION: Sequences and Uses Thereof

FILE REFERENCE: CL000284

CURRENT APPLICATION NUMBER: US/60/185,359

CURRENT FILING DATE: 2000-02-28

NUMBER OF SEQ ID NOS: 2926

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1293

LENGTH: 263456
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; TYPE: DNA
; ORGANISM: Drosophila
US-60-185-359-1293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: DNA
; ORGANISM: Drosophila
US-60-164-769-24606
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US-60-164-769-24606
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; LOCATION: 82, 192, 271, 409
; OTHER INFORMATION: a, t, c,
US-60-172-375-1200
                                                                                                                                                                                                                                                                                                                                                                                        Db 100504 cggc 100507
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Best Local S
Matches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/60/164,769
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 27328
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24606
LENGTH: 120625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24606, Application US/60164769
GENERAL INFORMATION:
APPLICANT: Venter, J. Craig
TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
TITLE OF INVENTION: Acid Sequences, Systems Containin the I
TITLE OF INVENTION: and Uses Thereof
FILE REFERENCE: CL000144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 42; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 totocatcotcottotcagotgotctgttctcgacagottcgggggaactgattccgc 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
mes 49; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 ggattgtcagctctccatcctccttctctcagctgtctctgtctctgacagcttcgggga 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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Pred. No. 1.3e+02;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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CURRENT APPLICATION NUMBER: US/60/133,875
CURRENT FILING DATE: 1999-05-12
NUMBER OF SEQ ID NOS: 2916
SOFTWARE: PERL PROGRAM
SEQ ID NO 1443
LENGTH: 310
TYPE: DNA
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-528-237-1293

; Sequence 1293, Application US/09528237
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; TITLE OF INVENTION: The Drosophila Genome, Primary Nucleic
; TITLE OF INVENTION: Acid Sequences, Systems Containing The Nucleic
; TITLE OF INVENTION: Sequences and Uses Thereof
; FILE REFERENCE: CL000284
; CURRENT APPLICATION NUMBER: US/09/528,237
; CURRENT ETLING DATE: 2000-03-17
                                                           ; OTHER INFORMATION: US-60-133-875-1443
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; ORGANISM: Drosophila
US-09-528-237-1293
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Best Local Similarity
Matches 42; Conserv
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1293
LENGTH: 263456
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   Query Match
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                                                                                                          FEATURE:
NAME/KEY: unsure
LOCATION: 2, 16, 119
OTHER INFORMATION: 6
                                                                                                                                                                                                                                                                                                                                APPLICANT: Garrow, Bonnie L.
APPLICANT: Mullahy, Sara J.
APPLICANT: Goralski, Thomas J.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM RAT LIVER
FILE REFERENCE: PZ-0118 P
                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 totocatootootoottotoagotgototgttotogacagottogggggaactgattoogc 73
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   32.98;
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Pred. No. 1.5e+02;
0; Mismatches 22;
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   Score 28
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Pred. No. 1.5e+02;
0; Mismatches 22;
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                                                                                                                unknown,
   6;
   DB
 83;
                                                                                                                or other
Length 310;
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RESULT 10
US-09-514-000-369/c
; Sequence 369, Application US/09514000
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US-60-168-139-2003
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US-09-514-000-6818/c
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; ORGANISM: Agrobacterium tumefaciens
US-09-514-000-6818

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GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequence And Uses Thereof
FILE REFERENCE: 38-21(15490)A
CURRENT APPLICATION NUMBER: US/60/168,139
CURRENT FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 3432
SEQ ID NO 2003
LENGTH: 4266
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GENERAL INFORMATION:
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15490)
CURRENT APPLICATION NUMBER: US/09/514,000
CURRENT FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 15034
SEQ ID NO 6818
LENGTH: 999
TYPE: DNA
CONTROL ACCEPTAGE 150751
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Best Local Similarity
Matches 47; Conser
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Best Local Similarity
Matches 47; Conserv
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                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                610 gattacgggctcaccttcctcggcctgctcggcatcgccattcccaacttcatgctggca 669
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                                                                                                                                                                    4 gattgtcagctctccatcctcctccttctcagctgctctgttctcgacagcttcggggaa
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Pred. No. 88;
0; Mismatches
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0; Mismatches
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Pred. No. 1.1e+02;
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Query Match
Best Local Similarity
"~+~hes 42; Conserve
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US-60-183-791-6260/c
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Agrobacterium tumefaciens Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15490)B
CURRENT APPLICATION NUMBER: US/09/514,000
CURRENT FILING DATE: 2000-02-23
NUMBER OF SEQ ID NOS: 15034
SEQ ID NO 369
LENGTH: 38536
TYPE: DNA
CONTROL OF SECURE OF SECURE
                                                                                                                                                                                                                                                                                                   Sequence 6260, Application US/60183791 GENERAL INFORMATION:
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SEQ ID NO 6260
LENGTH: 1454
TYPE: DNA
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Best Local Similarity
Matches 47; Conserv
APPLICANT: Bower, Stanley G.
APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: Xanthemonas campestris Genome
FILE REFERENCE: 38-10(15804)B
CURRENT APPLICATION NUMBER: US/80/183,791
CURRENT FILING DATE: 2000-02-22
NUMBER OF SEQ ID NOS: 18992
SEQ ID NO 6260
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APPLICANT: Hinkle, Gregory J.
TITLE OF INVENTION: Xanthomonas campestris Genome
FILE REFERENCE: 38-10(15804)A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 ttgtcagctctccatcctccttctcagctgctctgttctcgacagcttctggggaact 65
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Pred. No. 1.1e+02;
0; Mismatches 23;
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Pred. No. 1.
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1.5e+02;
hes 31;
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Sequence 33845, Application US/09531113
GENERAL INFORMATION:
APPLICANT: Byrum, Joseph R.
APPLICANT: Heck, Gregory R.
APPLICANT: La Rosa, Thomas J.
TITLE OF INVENTION: Nucleic Acid Molecules A
TITLE OF INVENTION: Plants:
FILE REFERENCE: 38-21(13761)B
CURRENT APPLICATION NUMBER: US/09/531,113
CURRENT FILING DATE: 2000-03-22
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          APPLICANT: Buehler, Robert E.
APPLICANT: Byrum, Joseph R.
APPLICANT: Gombs, Brian E.
APPLICANT: Heck, Gregory R.
APPLICANT: Heck, Gregory R.
APPLICANT: Melson, Donald E.
APPLICANT: Shukla, Hridayabhiramjam
APPLICANT: Shukla, Hridayabhiramjam
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ANI
TITLE OF INVENTION: PLANTS
FILE REFERENCE: 38-21(15444)B
CURRENT APPLICATION NUMBER: US/60/144,084
CURRENT FILING DATE: 1999-07-16
RUMBER OF SEQ ID NOS: 47776
                                                                                                                                                                                                                                                                                                        US-60-144-084-16459/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: 700892085H1 US-09-531-113-33845
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Best Local Similarity 77.3
Matches 34; Conservative
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Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                          Sequence 16459, Application US/60144084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 48629
SEQ ID NO 33845
LENGTH: 174
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NUMBER OF SEQ
SEQ ID NO 16459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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TYPE: DNA
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Pred. No.
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Pred. No. 1.1e+02;
0; Mismatches 23;
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89;
                                                                                               AND OTHER MOLECULES ASSOCIATED WITH
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; TYPE: DNA;
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3109-014-Q1-K1-A10
US-60-144-084-16459
                                                                                                                                                                                                                        SEQ ID NO 17798

LENGTH: 391

TYPE: DNA

ORGANISM: Glycine max

EEATURE:
COTHER INFORMATION: Clone ID: LIB3109-053-Q1-K1-D9
US-60-144-084-17798
Search completed: May 13, 2000, 15:18:39 Job time: 5212 sec
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Best Local Similarity 77.:
Matches 34; Conservative
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Best Local Similarity 77...
Matches 34; Conservative
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APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: NUCLEIC ACID MOLECULES
TITLE OF INVENTION: PLANTS
FILE REFERENCE: 38-21(15444)B
                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/60/144,084
CURRENT FILING DATE: 1999-07-16
NUMBER OF SEQ ID NOS: 47776
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Byrum, Joseph R.
Coombs, Brian E.
Heck, Gregory R.
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Shukla, Hridayabhiramjam
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77.3%;
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Pred. No. le+02;
0; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                 AND OTHER MOLECULES ASSOCIATED WITH
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Maximum DB seq length: 1000000
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1: /cgn2_6/ptodata/

2: /cgn2_6/ptodata/

3: /cgn2_6/ptodata/

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107.646 Million cell updates/sec
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/2/ina/6_COMB.seq:*
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US-08-619-5428-37
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US-08-901-200A-14
US-07-800-3548-13
US-07-981-703-10
US-07-981-703-10
US-08-147-023-28
US-08-1480-528A-7
US-08-155-343A-20
US-08-643-565A-20
US-08-447-570-28
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US-08-445-53A-20
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US-08-445-468A-20
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US-08-715-106-9
US-08-619-542B-34
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     8-445-468A-20
8-901-200A-7
8-449-700-28
Sequence 9, Appli
Sequence 3, Appli
Sequence 34, Appli
Sequence 36, Appl
Sequence 37, Appl
Sequence 11, Appl
Sequence 11, Appl
Sequence 10, Appl
Sequence 28, Appl
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Sequence 1, Appli	11,	Sequence 11, Appl	Sequence 11, Appl	Sequence 5, Appli	7, 2	20,	Sequence 20, Appl	-	-		Sequence 5, Appli	-	Sequence 20, Appl	•	-	Sequence 20, Appl	Sequence 28, Appl	

ALIGNMENTS

5	TYPE: Ducleic acid
	CHARACTERIS
9:	N FOR SEQ ID NO:
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6	TELEFAX: (516) 742-4366
343	TELEPHONE: (516
TTON:	TELECOMMINICATION INTERPRETATION:
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9992 (AU)	; APPLICATION NUMBER: PK9992
	; PRIOR APPLICATION DATA:
	; FILING DATE: 21-JUN-1991
6841 (AU)	LICATION NO
	PRIOR APPLICATION DATA:
	N: 435
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US/08/167,919A	; APPLICATION NUMBER: US/08/
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Plaza	T: 400 Garden City Pl
tt, Murphy & Presser	Scott,
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	R OF SEQUENCES: 14
THEREOF	OF INVENTION: AND USE
	TITLE OF INVENTION: A NOVEL
i.	ward, Larry
	: Wicks, Ian
ard J.	: Simpson, Richard
Σ.	
	GENERAL INFORMATION:
010/313W	. Sequence 9, Application 03/0818/919A
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Best Local Similarity 100.0%;
Matches 87; Conservative (
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                                TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 9:
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MEDIUM TYPE: Floppy disk
COMPUTER: LIBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TOPOLOGY: line
MOLECULE TYPE: 1
                                                                           NAME: D1G1g110, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 91:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                    APPLICATION NUMBER: PK9992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/167,919
FILING DATE: 18-APR-1994
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
SEQUENCE CHARACTERISTICS:
LENGTH: 3132 base pair
                                                                                                                                                                    FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: A NOVEL TITLE OF INVENTION: AND USE NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wicks, Ian
Ward, Larry D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilkinson, David
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100..3048
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Pred. No. 4.6e-21;
); Mismatches 0;
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; LOCATION: US-08-619-542B-34
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Best Local Similarity 100.0%;
Matches 87; Conservation
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APPLICANT: The Trustee:
APPLICANT: of New York
                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 324 base pairs
                                                                                                                                                                                                   NAME: White, John P.
REGISTRANICO NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/619,542
FILING DATE: June 21, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper &
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                                                FEATURE:
                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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LOCATION:
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                              NAME/KEY:
                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                      TELEFAX: (212)
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100..3048
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              12..311
                                                                                                                                                                                                                                                                                                                                                                       E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                             linear
                                                             peptide
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of the Americas
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Query Match
Best Local Similarity
Matches 38; Conserv

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Score 27.2; DB Pred. No. 0.6; 0; Mismatches

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Length 324;

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5438126-1/c
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APPLICANT: DEGROOT,
TITLE OF INVENTION:
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Best Local Similarity
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/83
FILING DATE: 03-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 405,342
FILING DATE: 11-SEP-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Re-lease #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1534 CTCCCA 1529
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                                                                                ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 42840-A-PCT-US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: METHOD FOR CONSTRUCTION OF NORMALIZED TITLE OF INVENTION: CDNA LIBRARIES
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                                                                                                                                                                         APPLICATION NUMBER: US/08/
FILING DATE: June 21, 1996
CLASSIFICATION: 435
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                                                   (212)
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                                                 (212) 278-0400
12) 391-0525
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HUMAN THYROID HORMONE RECEPTOR DNA
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Best Local Similarity
Watches 37; Conserve
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: Sequence 37, Application US/08619542B

: Patent No. 5830662
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                                                                                                     Matches
                                                                                                                 Query Match
Best Local
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FILING DATE: June 21, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 4284
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 323 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: L. York York
                                            275
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                                                                                                                                                                                       NAME/KEY:
LOCATION:
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62 aactgattccgcagccttcc 81
                                                                                                                Local
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TOPOLOGY: 11
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                 TELEFAX:
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                                                                                                  1 Similarity
46; Conserv
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1185 Avenue of the Americas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METHOD FOR CONSTRUCTION OF NORMALIZED
                                                                                                                29.48;
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                                                                                                                                                                                                                                                                                                                     37:
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Pred. No. 2.1;
0; Mismatches
                                                                                                  0;
                                                                                                              Score 25.6;
Pred. No. 2.
                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Version #1.30
                                                                                                                              DB
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                                                                                                  Indels
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                                                                                       Query Match
Best Local 9
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                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT AFFLICATION NUMBER: US/08/YUL, APPLICATION NUMBER: US/08/YUL, AFFLING DATE: 28-JUL-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THOMAS C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (508) 435-6951
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 435 9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
TITLE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                    NAME/KEY: misc_feature LOCATION: 1..950
                                                                                                                                                                                                                                 NAME/KEY: exon
LOCATION: 466..930
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                    NAME/KEY: exon
LOCATION: 204..393
OTHER INFORMATION:
                                                                                      Local
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                                                                   45; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
DEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES 1: 45 SOUTH STREET HOPKINTON
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OZKAYNAK, ENGIN
KUBERASAMPATH, THANGAVEL
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                                                                                    29.0%;
                                                                                                                                                                 /note= "hOP-2 genomic sequence"
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                                                                                                                                                                                                                                     /note-
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                                                                 Score 25.2; D
Pred. No. 4.2;
0; Mismatches
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Query Match
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US-07-800-364B-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/07800364B Patent No. 5688678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                MOLECULE TYPE: (
HYPOTHETICAL: NO
ORIGINAL SOURCE:
              FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony J.
TITLE OF INVENTION: Bone and Cartilage Inductive Proteins
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KAPINOS, Ellen J.
REGISTRATION NUMBER: 32,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1003 base pairs
TYPE: nucleic acid
                                                                                                                                                          POSITION IN UNITS: b
                                                                                                                                                                                                      IMMEDIATE SOURCE:
   LIBRARY: Human heart cDNA library stratagene catalog
   LIBRARY: #936208
                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 617-876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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                                                                                                          NAME/KEY:
LOCATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                            LOCATION:
                                                                           NAME/KEY:
                                                                                                                                                                                        CLONE:
                                                                                                                                                                                                                                                      TISSUE TYPE:
                                                                                                                                                                                                                                                              ORGANISM: Hopmo sapiens
                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: double
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hн38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                       GENOME:
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                               mRNA
                                                                                                       CDS
8..850
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                                                           mat_peptide
427..843
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           1..997
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SYSTEM: PC-DOS/MS-DOS
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Conservative

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Mismatches

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Indels

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Gaps

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29.0%; 57.7%;

Score 25.2; Pred. No. 4

DB 1; Length 1003;

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RESULT 9
US-07-989-847-11
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                 FEATURE:
                                                                                                                                                                                                               CLONE: hH38
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
LIBRARY: Human heart cDNA library stratagene catalog
LIBRARY: #936208
                                                                                                                                                                                                                                                                                                              ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: CI
                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Israel, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 617-876-1170
                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 GGTCCAGGAGCAGTCCAA 165
                                                                                                                                                        NAME/KEY:
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                                                                                                                                                                                                   UNITS:
                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1003 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Kapinos, Ellen J
REGISTRATION NUMBER: 32
                                                                                                                 LOCATION:
                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                     TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
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    Legal Affairs, Genetics Institute, Inc
87 CambridgePark Drive

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8..850
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                                                                     mRNA
1..997
                                                                                                              mat_peptide
427..843
                                                                                                                                                                                                                                                                                  Human Heart
                                                                                                                                                                                                                                                                                                                                          cDNA to mRNA
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 29.0%;
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Score 25.2; DB Pred. No. 4.3;
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             Length 1003;
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GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT:
             FILING DATE: 20-AUG-
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                   FILING DATE: 04-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 6:
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 6: FILING DATE: 04-DEC-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 28-JAN-PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 8
FILING DATE: 20-DEC-1991
PRIOR APPLICATION DATA:
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                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                         FILING DATE: 21-NOV-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER
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                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 GGTCCAGGAGCAGTCCAA 165
                                                                                                                  APPLICATION NUMBER: US 5 FILING DATE: 18-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: UFILING DATE: 19920221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC
OPERATING SYSTEM:
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                                                                        APPLICATION NUMBER: US 579,865 FILING DATE: 07-SEP-1990
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                                                                                                                                                                  FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE:
APPLICATION NUMBER:
                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTACAAGGTGCCCAGCATCCACCTGCTCAACAGGACCCTCCACGTCAGCATGTTCCAGGT 147
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                                                                       DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   READABLE FORM:
TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MASSACHUSETTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/07841646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KUBERASAMPATH, TI
RUEGER, DAVID C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OZKAYNAK, ENGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPPERMANN, HERMANN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TESTA, HURWI
STATE STREET
                             20-AUG-1990
                                                                                                                                                              18-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                       28-JAN-1992
                                                                                                                                                                                                                                                                                                                                           22-FEB-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OSTEOGENIC DEVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HURWITZ & THIBEAULT
                                                                                                                                                                                                                                                                    US 621,849
                                                                                                                                                                                                                                                                                                                US 621,988
                                                                                                                                                                                                                                                                                                                                                         US 660,162
                                                                                                                                                                                                                                                                                                                                                                                                        US 827,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                   US 810,560
                                            US 569,920
                                                                                                                                US 599,543
                                                                                                                                                                            US 600,024
                                                                                                                                                                                                                         US 616,374
US 483,913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/07/841,646
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FILING DATE: 17-OCT-PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 422,613 FILING DATE: 17-OCT-1989

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US-07-901-703-10
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                           Patent No. 5344654
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/07901703 patent No. 5344654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION UNMER: US 315,342
FILING DATE: 23-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 232,630
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 179,460
FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 617/248-7100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1723 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: EXCHANGE PLACE, 53 STATE STREET
                                                                                                                                                                                                            TITLE OF INVENTION: PROSTHETIC DEVICES HAVING ENHANCED TITLE OF INVENTION: OSTEOGENIC PROPERTIES NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                    APPLICANT: RUEGER, DAVID C
APPLICANT: KUBERAŞAMPATH, THANGAVEL
APPLICANT: OPPERMANN, HERMANN
APPLICANT: OPERMANN, ENGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INAME/KEY: CDS
LOCATION: 490..1696
OTHER INFORMATION: /f
OTHER INFORMATION: /F
OTHER INFORMATION: /r
                                                                                                                STREET: E-STON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               993 GGTCCAGGAGCAGTCCAA 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       933 TTACAAGGTGCCCAGCATCCACCTGCTCAACAGGACCCTCCACGTCAGCATGTTCCAGGT 992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match 29.0%;
Local Similarity 57.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98
                                                                            COUNTRY: USA
ZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE TYPE: HIPPOCAMPUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: NUCLEIC ACID
STRANDEDNESS: Sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 ttgtcagctctccatcctccttcttcagctgctctgttctcgacagcttccggggaact 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gattccgcagccttccaa 83
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OZAKAYNAK, ENGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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/product= "hOP2-PP"
/note= "hOP2 (cDNA)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRP-001CP6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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; LOCATION: 490..1696
; OTHER INFORMATION: /function= "OSTEOGENIC PROTEIN"
; OTHER INFORMATION: /product= "hOP2-PP"
; OTHER INFORMATION: /note= "hOP2 (cDNA)"
US-07-901-703-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 28,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 29.0%;
Best Local Similarity 57.7%;
                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: OPPERMANN, HERMANN
APPLICANT: OFFICE OF OFFICE OF OFFICE OFFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1723 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CORIGINAL SOURCE:
ORGANISM: Homo
TISSUE TYPE: H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/07/901,703
FILING DATE: 19920616
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: mpcm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: PITCHER ESQ, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: STK
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7000
                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                    PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                         STREET: 53 ST
CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single TOPOLOGY: linear
                                                      APPLICATION NUMBER: US/08/147,023 FILING DATE: 21-FEB-1992
                                                                                                                                                                                                                                 COUNTRY: U.S.A.
                                                                                                                                                                                                                                                         STATE:
APPLICATION NUMBER:
                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 ttgtcagctctccatcctccttctcagctgctctgttctcgacagcttcggggaact 65
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5468845
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                                                                                                                                                                                                                                                                                           E: TESTA, HURWI
53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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490..1696
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E: HIPPOCAMPUS
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                                                                                                                                                                                                                                                                                                               HURWITZ & THIBEAULT
US 810,560
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Pred. No. 5.1;
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PRIOR APPLICATION DATA:

APPLICATION NUMBER:

04-DEC-1990

US 621,988

APPLICATION NUMBER: US 660,162 FILING DATE: 22-FEB-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FILING DATE: 28-JA

US 827,052

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Query Match
Best Local Similarity
"~*~hes 45; Conserve
                                                                                                          US-08-147-023-28
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/248-7100
TELEFAX: 617/248-7100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 315,342
FILING DATE: 23-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 579,865 FILING DATE: 07-SEP-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 599,543
FILING DATE: 18-OCT-1990
                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 08-APR-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 2:
FILING DATE: 15-AUG-1988
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 483,913 FILING DATE: 22-FEB-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 569,920 FILING DATE: 20-AUG-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 621,849 FILING DATE: 04-DEC-1990 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 18-OCT-
PRIOR APPLICATION DATA:
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                                                                                                                         NAME/KEY: CDS
LOCATION: 490..1696
OTHER INFORMATION: /:
OTHER INFORMATION: //
OTHER INFORMATION: //
                                                                                                                                                                                                                                                                                                                           LENGTH: 1723 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: CRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: PITCHER, EDMUND REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 422,613 FILING DATE: 17-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 60 FILING DATE: 18-OCT-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 616,374 FILING DATE: 21-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 179,460 FILING DATE: 08-APR-1988
                                                                                                                                                                                                                                   TISSUE TYPE: HIPPOCAMPUS
                                                                                                                                                                                                                                                          ORGANISM:
                  Conservative
                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                            linear
                                  29.0%;
57.7%;
                                                                                                                         /function= "OSTEOGENIC PROTEIN"
/product= "hOP2-PP"
/note= "hOP2 (cDNA)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US 232,630
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               Score 25.2; DI
Pred. No. 5.1;
0; Mismatches
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                                                 DB 1; Length 1723;
                 33;
               Indels
               0
               Gaps
               0
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
US-08-206-864-3
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US-08-206-864-3
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                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 530
PRIOR APPLICATION UMBER: US 08/027
APPLICATION NUMBER: US 08/027
FILING DATE: 04-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/841
FILING DATE: 21-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: PITCHER, EDMUND R
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                             TELEFAX: 617/248-7100 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                       MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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ADDRESSEE: PATENT ADMINISTRATOR/CREATIVE BIOMOLECULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TITLE OF INVENTION: RECOMBINANT OSTEOGENIC PROTEIN PRODUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 6
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ZIP: 01748
                                                                   NAME/KEY:
LOCATION:
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                                                                                                                      ORGANISM: Homo sapiens
TISSUE TYPE: HIPPOCAMPUS
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                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                            STRANDEDNESS: single
                                                                                                                                                                                                                            TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                     490..1696
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          /function= "OSTEOGENIC PROTEIN"
/product= "hOP2-PP"
/note= "hOP2 (cDNA)"
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Best Local Similarity 57.7 Matches 45; Conservative

57.7%;

Pred. No. 5.1; 0; Mismatches

33;

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Best Local Similarity
Matches 45; Conserv
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Patent No. 5650276
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER: COMPUTER: PM PC COMPUTER: DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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APPLICANT:
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NAME: PITCHER ESq., EDMUND R.
REGISTRATION NUMBER: 27,829
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TITLE OF INVENTION: MORPHOGENIC PROTEIN SCREENING METHOD
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
STREET: 45 SOUTH STREET
                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: CRITELECOMMUNICATION INFORMATION: TELEPHONE: (508) 435-9001
                                                                                                                                                                                                                                                                                      MOLECULE TYPE: cDNA
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                                                                                                                                                                                                                                                                                                    LENGTH: 1723 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/278,729A FILING DATE: 20-JUL-1994
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LOCATION: 490..1695
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GGTCCAGGAGCAGTCCAA 1010
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OZKAYNAK, ENGIN
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NAME/KEY: CDS
LOCATION: 490..1696
COTHER INFORMATION: /f
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US-08-480-528a-7
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                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1723 base pairs
TYPE: nucleic acid
STRANDENESS: single
                                                                                                                                      Matches
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Best Local Similarity
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APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/08/480,528A
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
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ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
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                                                                  933 TTACAAGGTGCCCAGCATCCACCTGCTCAACAGGACCCTCCACGTCAGCATGTTCCAGGT 992
                         66 gattccgcagccttccaa 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: FENTON ESq., GILLIAN M. REGISTRATION NUMBER: 36,508
REFERENCE/DOCKET NUMBER: CRP-
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GGTCCAGGAGCAGTCCAA 1010
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KUBERASAMPATH,
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                                                                                                                                      Conservative
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Search completed: May 15, 2000, 12:05:03 Job time: 4422 sec

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Title:
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195.849 Million cell updates/sec
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cellular res	production and/or function of pre-B, 1 analogues have activity in transducing	the epit	urs of h	essed in	m 6; Fig	therapy etc.	eins in	III-A4 - is		93-0363	AD, Simpson	L-) HALI	EC-1991;	UN-1992;	07-JAN-1993.	00425-A		peptide		peptide		_reacure		ignal_peptide	i-	i		i	sey	hetic.	ligand;	a-1; JM;	elk-like	er: expi	24-MAY-1993 (first)	13;	13 stand	ш		ć	24 23.8						
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growth and/or differentiation 711 C; 759 G; 7	agents in module and T cells.	recepto		ell lines and in			B and T cell function, in can	, useful for			н	er El				Ted HEV brotein #7.		ed mey brocern *T	0d upv pro+045 #		ial transmembrane region"								fiers		growt	ceptor	cell; T; tumour; lymphoid; LK63;	acellul					ALIGNMENTS		V74538 X39853						
tion. 774 T;		ymidine kinase	4	a number of			n cancer	antipody ating													3										on; ss.	kinase;	; LK63;	TAX.						Carro	Staphylococcus aur		Pumpkin ent-kauren	creted	Dermatomyositis sp C-Delta-1 gene (al	Human glial tumour) }

Query Match 100.0%; Best Local Similarity 100.0%; Matches 87; Conservative 0;

Score 87; DB 1; 1 Pred. No. 3.9e-19; Mismatches 0;

Length 3132; ; ; Indels

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RESULT
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Pr A plant ferritin gene induced in acidic growth conditions

Pr plants, improves resistance to acidic growth conditions

Pr plants, improves resistance to acidic growth conditions

PS Claim 1; Page 6-7; 9pp; Japanese.

CC Gris sequence represents a plant ferritin gene. The plant ferritin

CC gene, whose production is induced in acidic soil, is involved in the

CC coccurrence of disorders in a plant caused by acidic conditions.

CC This gene can be used for breeding of plants highly resistant to acidic

CC soil. The cDNA or its fragment can also be used for diagnosis of a

CC glant planted in acidic soil by determining the expression of ferritin

CC in it. Ferritin can be expressed excessively by introducing the cDNA

CC of the invention into a plant in the sense direction to reinforce the

CC resistance of the plant to acidic soil. Therefore acidic soil which could

CC not the utilised for agricultural purposes can be utilised by the
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 41
  V57542 standard;
V57542;
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WPI; 97-344897/32.
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/note= "PolyA_site"
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WP Sequence wp V21209
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V21209_09/c
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Claim 2; Pages 26-33; 45pp; English.

This represents a cDNA from BAC bk206c7 encoding a partial sequence of a human calcium channel subunit alpha-1. The invention provides isolated CNA fragments coding for novel calcium channel subunits alpha-II and alpha-IH. An eukaryotic cell transiently or stably transformed with an expression vector containing the calcium subunits encoding DNA fragments can be used for expressing the calcium channel. The cells are optionally further transformed to express alpha 2 delta or beta calcium channel or beta the proteins. The transformed cells are useful for identifying compounds capable of acting as agonists or antagonists for the alpha-II calcium channel. The nucleic acid sequences can be used in histological assay to determine the tissue distribution of the novel calcium channel
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Best Local S
Matches 35
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P Fragment Nar
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P V21209_01
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P V21209_03
P V21209_04
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03-SEP-1998; CA0173.
27-FEB-1998; US-030482.
25-FEB-1998; US-039204.
(NEUR-) NEUROMED TECHNOLOGIES I
Baillie DL, Snutch TP;
WPI; 98-481203/41.
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Query Match

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Human; secreted protein; fusion protein; gene therapy; protein therapy;

diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;

developmental abnormality; foetal deficiency; blood; allergy; renal; ds;

inflammation; ischaemic shock; Alikheimer's disease; restenosis; AIDS;

cognitive disorder; schizophrenia, prostate; obesity; osteoclast; thymus;

osteoporosis; arthritis; testis; lung; thyroiditis; thyroid digestion;

endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
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V84466;
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PR 05-SEP-1997, US-05766.
PR 05-SEP-1997, US-05766.
PR 05-SEP-1997, US-057762.
PR 05-SEP-1997, US-057762.
PR 05-SEP-1997, US-057762.
PR 05-SEP-1997, US-057763.
PR 05-SEP-1997, US-057763.
PR 06-UN-1997, US-04889.
PR 06-UN-1997, US-04971.
PR 06-UN
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Query Match 29.9%; Score 26; DB 1; Length 1866; Best Local Similarity 59.5%; Pred. No. 11; Matches 44; Conservative 0; Mismatches 30; Indels 0; Gaps

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RESULT

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Q951

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Best Local S
Matches 41
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11-SEP-1989; US-405342.

03-FEB-1992; US-830766.

(ARCH-) ARCH DEV CORP.

Degroot LJ, Nakai A;

WPI; 95-274923/36.
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01-AUG-1995.
11-SEP-1989;
11-SEP-1989;
03-FEB-1992;
                                                                                                Human secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer; disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus; osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prods. for use in analysis, assays and therapeutic agents Claim 1; Fig 1; 7pp; English.
Q95:10 encodes R78318 human thyroid hormone receptor alpha-1 (hr. alpha-1). The nucleic acid can be used to develop prods. for use analysis assays and therapeutic agents. hTR-alpha-1 can be used tests for thyroid function, or for producing antibodies for use affinity purificn., detection and quantification.

Sequence 1893 BP; 461 A; 531 C; 551 G; 350 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-MAR-1996 (first entry)
106-MAR-1996 (first entry)
107-MAR-1996 (first entry)
108-MAR-1996 (first en
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                                        Homo sapiens.
W09842738-A1.
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25-MAR-1999
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/*tag=
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agents
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PS Claim 1; Page 215; 385p; English.

CThis sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number, and the clone it is derived from, are detailed in the descriptor line. The gene can be used to generate fusion proteins by linking to the gene to human immunoglobulin Fc portion (e.g. x00602) for increasing the stability of the fused protein as compared to the human protein only.

CC compared to the human protein only.

CC The invention relates to 87 novel genes and their fragments (nucleic acid sequences: x00611-x00724; amino acid sequences w67807-w68004) which care useful for preventing, treating or ameliorating medical conditions can be diagnosed by determining the amount of the new polypeptides in a sample cor by determining the presence of mutations in the new polypucleotides. Specific uses are described for each of the 87 polynucleotides, based on which tissues they are most highly expressed in (see x00611 for described contents).
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Best Local
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Greene JM, Hu JS,
Rosen CA, Ruben 9
WPI; 99-070066/08
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30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
30-MAY-1997;
                                             Homo sapiens.
Key
CDS
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30-MAY-1997;
21-MAR-1997;
21-MAR-1997;
21-MAR-1997;
21-MAR-1997;
30-MAY-1997;
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30-MAY-1997;
05-AUG-1997;
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                                                                                                                  Human; long ch inhibitor; ss.
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J5-AUG-1997; US-054804.

(HUMA-) HUMAN GENOME SCI INC.

Brewer LA, Duan R, Ebner R, Ferrie Al
Brewer LA, Duan R, Lafleur DW, Moore
                                                                                                                                                          Human derived
                                                                                                                                                                                     T94563;
22-APR-1998
                                                                                                                                                                                                                                  T94563 standard;
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30-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                44 TGTAAGGCCCGCAGCTCCCGCCAGCTCCCGCGGACTSCTGCCGCCTCCTTACCATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                          37;
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US-048069
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US-04818
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                                                                                                                           (first entry)
d long chain DNA novel gene.
chain DNA; antibody; nervous
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                                          Location/Qualifiers
1. .1269
/product=
                          /*tag=
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"long chain DNA protein"
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W, Moore PA, Ni J, Olsen
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Pred. No. 9.9;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89
                                                                                                                                       nervous
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                                                                                                                                   disorder; detection;
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                                          Matches
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03-APR-1996; JP-081304.
(ASAH ) ASAHI KASEI KOGYO K
KATO C, Takada Y;
WPI: 97-503103/46.
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03-APR-1996; JF-081304,
(ASAH ) ASAHI KASEI KOGYO K
KATO C, Takada Y;
WPI; 97-503103/46.
                                                                                                     Human long chain DNA and antibodies which bind to the peptide(s) - is potentially useful in treating nervous disorders Claim 4; Page 92-93; 109pp; Japanese.

The present sequence represents human derived long chain DNA comprising at least a peptide-encoding region. Peptides encoded by the human derived long chain DNA, may be used for detecting substances which bind to the peptides, and for detecting substances which suppress or inhibit binding to these peptides. The peptides and their inhibitors are potentially useful in treating nervous disorders.

Sequence 1562 BP; 318 A; 506 C; 389 G; 349 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human long chain DNA and antibodies which bind to the peptide(s) - is potentially useful in treating nervous disorders Claim 3; Page 91-92; 109pp; Japanese.

The present sequence represents human derived long chain DNA comprising at least a peptide-encoding region. Peptides encoded by the human derived long chain DNA, may be used for detecting substances which bind to the peptides, and for detecting substances which suppress or inhibit binding to these peptides. The peptides and their inhibitors are potentially useful in treating nervous disorders.

Sequence 1269 BP; 263 A; 413 C; 285 G; 308 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                          22-APR-1998 (first entry)
Human derived long chain DNA novel gene.
Human; long chain DNA; antibody; nervous disorder; detection;
inhibitor; ss.
                                                                                                                                                                                                                                                         P-PSDB; W32797.
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09-OCT-1997.
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T94564;
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cagototocatootoottootoagotgototgttotogacagottoggggaactgatt 69
                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens
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                                            44;
                                                      Similarity
                                          Conservative
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168. .1439
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/product= "long chain DNA protein"
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                                                     29.2%;
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                                       Score 25.4; D
Pred. No. 16;
0; Mismatches
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Pred. No. 15;
0; Mismatches
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Similarity 57.

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                                                                      Problement the control of the process of the sequence is that encoding the human bone morphogenetic protein CC BMP-8. It may be used in the product of a recombinant heterodimeric CC protein having bone stimulating activity. This heterodimer is CC encoded by a sequence encoding BMP-2 or BMP-4 or a fragment and a CC sequence encoding a second protein or fragment, BMP-8. It may be CC used in compsns. for wound healing, tissue repair, and in similar CC compsns. which have been indicated for the use of individual BMPs. CC Increased potency of the heterodimer over individual BMPs may permit CC induces cartilage and/or bone growth in circumstances where bone CC induces cartilage and/or bone growth in circumstances where bone CC fractures and cartilage defects in humans and other animals. The CC contributes to the repair of congenital, trauma induced or oncologic resection induced craniofacial defects, and also is useful in cosmetic suspens and in other tooth repair processes. It may also be useful in the treatment of periodontal contributes and ulcers) and related tissue repair, and may increase neuronal survival and be useful in the transplantation and treatment of conditions exhibiting a decrease in neuronal survival. It may be useful in the transplantation and treatment of combined with other agents beneficial to the bone and/or cartilage defect, wound or tissue in question, e.g. EGF, PDGEF, TGF-alpha, Sequence 1002 BP; 196 A; 330 C; 285 G; 191 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant hetero-dimeric BMP proteins - are useful in bone defects, healing bone injury and in wound healing
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US-787496.
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427. .843
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1. .997
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8. .850
                29.0%;
57.7%;
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  osteoporosis; burns; incisions; ulcers;
  ease; fracture reduction; cartilage growth;
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Score 25.2; I
Pred. No. 17;
0; Mismatches

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                              Length 1002;
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GGTCCAGGAGCAGTCCAA 165 gattccgcagccttccaa

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Best Local S
Matches 45
                                                                               Q3894b; (2014) (first entry)
21-JUL-1993 (first entry)
Human osteogenic protein 2 (hOP-2) gene.
Bone; loss; increase; fracture; post-menopausal; senile;
osteoporosis; hyperparathyroidism; skeletal microstructure defects;
chronic renal failure; kidney disease; osteomalacia, vitamin D;
chronic renal failure; kidney disease; osteoporosis; Paget's disease;
'fillowy-induced osteopenia, osteoporosis; Paget's disease;
'fillowy-induced osteopenia, osteoporosis; Paget's calcium;
                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure: Page 102-104; 132pp; English.

Mature hOP2 is one of the preferred known morphogens which can be used in the manufacture of pharmaceuticals for inducing non-chondrogenic mammalian tissue growth, progenitor cell proliferation and hepatic tissue growth and for maintaining the phenotypic expression of differentiated cells in a mammal. Morphogenic compositions of the invention can also be used to treat blood disorders and impaired or lost immune function. Morphogens sharing at least 70% homology with hOP2 are included.

Sequence 1723 BP; 265 A; 624 C; 576 G; 258 T;
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Q28737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Compsns. for increasing progenitor morphogen to induce proliferation, neoplastic growth, inducing tissue
W09305751-A
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                                                               Homo
                                                                           bone mass;
phosphate;
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                                                                                                                                                                                                                                                                                                             TTACAAGGTGCCCAGCATCCACCTGCTCAACAGGACCCTCCACGTCAGCATGTTCCAGGT
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1991; US-667274.
CREATIVE BIOMOLECULES INC.
                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                           metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              morphogenic protein.
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                                     Location/Qualifiers
490. .1696
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57.7%;
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Pred. No. 19;
0; Mismatches
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28-AUG-1992; U07432.
30-AUG-1991; US-752764.
30-AUG-1991; US-752857.
30-AUG-1991; US-752861.
31-YUL-1992; US-923780.
(CREA-) CREATIVE BIOMOLECULES INC.
                                                                             WO9304692-A.
18-MAR-1993;
28-AUG-1992; U07358.
30-AUG-1991; US-752764.
30-AUG-1991; US-752861.
30-AUG-1991; US-753059.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      other kidney diseases, osteomalacia, vitamin D deficiency-induced osteopenia or osteoporosis, postmenopausal or senile osteoporosis, hyperparathyroidism and Paget's disease. The methods can be used for protecting individuals at risk for loss of bone mass such as postmenopausal females, aged individuals and individuals undergoing dialysis. The loss of bone mass may result from an imbalance in bone resorption or bone formation, an imbalance of calcium or phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that encoding human osteogenic protein 2 (hop-2) a morphogenically active protein which may be used as part of a method for treating a bone fracture or a disease which causes or results in bone fractures or other defects in skeletal microstructure. Such diseases include chronic renal failure and
                       Cohen CM, Kuberasampath T, Pang RHL, Rueger DC, Smart WPI: 93-100652/12.
                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                    morphogenic; osteogenic protein; developmental cascade; hOP-2;
inflammation; anti-inflammatory; Transforming Growth Factor;
TGF-beta super-family; hippocampus; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of morphogenic or in-vivo morphogenic-stimulating agent - to prevent bone loss or increase, used for treating bone fractures,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cohen CM, Kuberasampath T,
Pang RHL, Rueger DC, Smart
WPI; 93-117208/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     post-menopausal or senile osteoporosis, h
Disclosure; Page 115-117; 162pp; English.
Morphogen-induced modulation of inflammatory response -
               P-PSDB; R33410
                                                  Cohen CM,
                                                                                                                                                                                       mat_peptide
                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                              Human OP-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            metabolism,
                                                                   (CREA-) CREATIVE BIOMOLECULES INC
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1279.
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Pred. No. 19;
0; Mismatches
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                                                     Oppermann
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                                                     Ozkaynak
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                                                                                                                                                                           PT Screening cpds: to determine ability to modulate effective concn.

PT of a morphogen - by assaying test tissue type cells for parameter indicative of a prodn. level change of morphogen

PT indicative of a prodn. level change of morphogen

PS Disclosure; Page 95-97; 132pp; English.

CC This sequence encodes the human morphogen hOP2, isolated from the CC hippocampus. This morphogen is inactive when reduced but is active CC as an oxidised homodimer and when oxidised in combination with other CC morphogens. These morphogens are capable of stimulating proliferation CC of progenitor cell, stimulating the differentiation of progenitor cells, stimulating the proliferation of differentiated cells and CC supporting the growth and maintenance of differentiated cells, including the redifferentiation of transformed cells. These morphogens may also be capable of inducing redifferentiation of CC committed cells under appropriate environmental conditions.

Sequence 1723 BP; 270 A; 624 C; 572 G; 257 T;
                                                                                                   Query Match
Best Local S
Matches 45
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Best Local S
Matches 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-MAR-1993.
28-AUG-1992;
30-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          resulting tissue damage, e.g. in autoimmune diseases, diabetes, asthma, ischemia reperfusion injury, etc.
Claim 26; Page 119-121; 165pp; English.
Human osteogenic protein (OP)-2 is a preferred morphogen for use in treating tissue damage in e.g. inflammatory disease, autoimmune disease, arthritis, psoriasis, dermatitis, diabetes and emphysema.

Proteins having at least 70% homology with OP-2 amino acid sequences can also be used. See R33400 for mature hOP-2.

Sequence 1723 BP; 266 A; 625 C; 574 G; 258 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rueger DC, Smart Tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Morphogen hOP2 coding sequence.
Morphogen; homodimer; stimulate; proliferation; progenitor cell;
differentiation; growth; redifferentiation; transformation; huma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CREA-) CREATIVE BIOMOLECULES INC. Cohen CN, Kuberasampath T, Opper
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committed cells; hippocampus; ss.
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Matches 45
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New pure mammalian osteogenic proteins - induce cartilage and endochondral bone formation when in association with a matrix Claim 26; Columns 143-148; 128pp; English.

The osteogenic protein when in association with a matrix can induce at the locus of an implant the full development cascade of endochondral bone formation including vascularisation, mineralisation and bone marrow differentiation. The osteogenic protein can also be used to repair both bone and cartilage in the treatment of osteoarthritis. This sequence encodes the pre-proform of the protein.

Sequence 1723 BP; 265 A; 624 C; 577 G; 257 T;
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Q53155;
Q6-JUN-1994
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Osteogenic protein; bone; cartilage; matrix; osteoarthrit.
repair; vascularisation; mineralisation; differentiation;
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07-SEP-1990;
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-69.052 Million cell updates/sec
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LOCALLON/Qualifiers
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IRARTAAGYGINSRKFEFETSPDSFSISGESSQVYMLAISAAVIILLTVVITVLIGR
FCGYKSKHGADEKRLHFGNGHLKLPGLRTYVDPHTYEDPTQAVHEFAKELDATNISII
KVVGAGEFGEVCSGRLKLPSKKEISVAIKTLKYGYTEKQRTDFLGEASIMGQTDHDI
IRLEGVVTKSKPVMIVTEYMENGSLDSFLRKHDAQFTVIQLLGNLRGIASGMKYLSDM
GYVHRDLAARNILINSNLVCKYSDFGLSRVLEDDPEAAYTTRGGKIPIRWTSPEAIAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
100. .3051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETQSKNGPVPV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSOSLVEVRGSCVNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQACRPG
FYKALDGNMKCAKCPPHSSTQEDGSMMCCENNY FRADKDPSMCTRPPSS PRNYI
NINETSVILDWSWPLDTGGRKDVTFNIICKKCGWNIKQCEPCSPNVRRLPRQFGLTNI
TYTYTDLLAHTNYTFEIDAYNGVSELSSPPRQFAAVSITTNQAAPSPVLTIKKDRTSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mdcqlsillllscsvldsfgelipqpsnevnlldsktiqgelgw
ISYPSHGWEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFT
LRDCNSIPLVLGTCKETFNLXYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDR
ILKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPETVKNLAMEPDTVPM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MLDCWQKDRNNRPKFEQIVSILDKLIRNPGSLKIITSAAARPSNLLLDQSNVDISTFR
TTGDWLNGVRTAHCKEIFTGVEYSSCDTIAKISTDDMKKVGVTVVGPQKKIISSIKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKFTSASDVWSYGIVLWEVMSYGERPYWEMSNQDVIKAVDEGYRLPPPMDCPAALYQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAA01906.1"
/db_xref="GI:1247487"
                                                                         GI:2830140
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                                                                                                                          3132 bp
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Pred. No. 2.6e-18;
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REFERENCE
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FEATURES
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KEYWORDS
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HUMHEK
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Best Local :
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Boyd, A.W., Simpson, R.John, Wicks, I., Ward, L.David and Wilkin Method of screening for ligands to a receptor-type tyrosine Patent: US 5674691-A 9 07-OCT-1997;
Location/Qualifiers
1. .3132
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Homo sapiens lymphoid tumor cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wicks,I.P., Wilkinson,D., Salvaris,E. and Boyd,A.W. Molecular cloning of HEK, the gene encoding a receptor kinase expressed by human lymphoid tumor cell lines Proc. Natl. Acad. Sci. U.S.A. 89 (5), 1611-1615 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3149)
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                                                     /product="receptor protein kinase"
/protein_id="AAA58633.1"
/protein_id="AAA58633.1"
/db_xref="G:183932"
/db_xref="G:183932"
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ISYPSHGWEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFT
LRDCNSIPLYLGTCKETFNLYYMESDDDHGYKFREHOFTK.1D7IAADESFTQMDLGDR
ILKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVVRVFKKCPFTVKNLAMFPDTVPM
DSQSLVEVRGSCVNNSKEEDPPRMYCSTEGEMLVPIGKCSCNAGYEERGFMCQACRPG
FYKALDGNMKCAKCPPHSSTQEDGSMNCRCENNYFRADKDPSMACTRPPSSPRNVIS
NINETSVILDMSWPLDTGGRKDVTFNIICKKCGWNIKQCEPCSPNVRFLPRQFGLTNT
TVTVTDLAHTHNYTEEIDAVMGVSELSSPPRQFAAVSITTNQAAPSPULTIKKRRTSR
NSISLSWQEPEHPNGIILDYEVKYYEKQEQETSYTILARRGTNVTISSLKPDTIIVFQ
IRARJAAGYCTNSKREEFETSPDSFSISGESSQVVMALAISAAVAIILLTVVIVILIGR
FCGYKSKHGADEKRLHFGNGHLKLPGLRTYVDPHTYEDPTQAVHEFAKELDATNISD
KVVGAGEGEFGVGSGLIKLPSKKEISVALKTLKVGYTEKQREDFLGEASIMGQEPHPNI
IRLEGVVTKSKPVMIVTEYMENGSLDSFLRKHDAQFTVIQLVGMLRGIASGMKYLSDM
GSVHRDLAARNILINSKLVCKYSDFGLSRVLEDDDEAAYTRGGKIPIRWTSPEAIAY
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709 c 761 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="HEK"
101. .3052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_line="LK63"
TTGDWLNGVRTAHCKEIFTGVEYSSCDTIAKISTDDMKKVGVTVVGPQKKIISSIKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="HEK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="lymphoid tumor" | 101. .3052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine kinase (HEK) mRNA,
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Pred. No. 2.6e-18;
Mismatches 0;
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polyA_signal
polyA_site
BASE COUNT 578
ORIGIN
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Best Local S
Matches 87
                                                           Query Match
Best Local Similarity
Matches 71; Conser
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gaactgattccgcagccttccaatgaa 87
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 2032)
Sajjadi, F.G., Pasquale, E.B. and Subramani, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M68515.1 GI:454828
receptor tyrosine kinase.
Mus musculus (strain IRC x Swiss Webster) 11.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identification of a new eph-related receptor tyrosine kinase from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor leaf of the receptor 3, 769-778 (1991)
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37; Conservative
                                                                                                                                             578
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                                                           70.6%; ilarity 81.6%; Conservative
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Location/Qualifiers
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                                                                                                                                                                                                LRDCNSIPLVLGTCKETFNLYYMESDDHGVKFREHQFTKIDTIAADESSTQMDLGDRI
LKLNTEIREVGPVNKKGFYLAFODVGACVALVSVRYYFKKCPFTVKNLAMFPDTVPMD
SQSLVEVRGSCVNNSKEEDPPRNYCSTGGEWLVPIGKCTCNAGYEERGFICQACRPGF
YKASDGAAKCAKCPFHSSTQEDGSMNCRCENNYFRAEKDPPSMACARPPSAPRNVISN
INETSVLLDWSNPLDTGGRKDITFNIICKKCGWNVRQCEPCSBNVRFLPRQLGLTNTT
VTVTDLLAHTNYTFEIDAVNGVSELSSPPRQYAAVSITTNQAAPSPVMTIKKDRTSRN
SISLSWQEPEHPNGIILDYEWXYQKQEQETSYTILRARGTNVTISSLKPDTTYVFQI
                                                                                                                                                           RARTAAGYGTNSRKFEFETSPDCMYYFSF" 2010. .2015
                                                                                                                                                                                                                                                                                                                                                                                                                   /organism-"Mus musculus"
/strain-"IRC x Swiss Webster"
/db_xref-"taxon:10090"
/dev_stage-"11.5 day embryo"
                                                                                                                                                                                                                                                                                                   /translation="MDCHLSILVLLGCCVLSCSGELSPQPSNEVNLLDSKTIQGELGW
                                                                                                                                                                                                                                                                                                                               /protein_id="AAA39522.1"
/db_xref="GI:454829"
                                                                                                                                                                                                                                                                                                                                                            'product="Mek4 secreted"
                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                   'tissue_type="embryo"
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                                                      Score 61.4; DI
Pred. No. 5.2e<sup>o</sup>
0; Mismatches
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Pred. No.
                                                                                                                                             460
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                                                                      DB 12;
.2e-10;
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                                                                                       2032;
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1 atggattgtcagctctccatcctcctccttctcagctgctctgttctcgacagcttcggg 60

Matches

Conservative

0;

Indels

0;

Gaps

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JOURNAL
MEDLINE
REFERENCE
AUTHORS
TITLE
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AUTHORS
TITLE,
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SOURCE
ORGANISM
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Li,Y.Y., McTiernan,C.F. and Feldman,A.M.
Direct Submission
Submitted (01-SEP-1996) Cardiology, University of Pittsburgh,
Lothrop Street, Pittsburgh, PA 15213, USA
On Apr 18, 1997 this sequence version replaced gi:1698721.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNU69278
Rattus no
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IL-1 beta alters the expression of the receptor tyrosine kinase gene r-EphA3 in neonatal rat cardiomyocytes
Am. J. Physiol. 274 (1), H331-H341 (1998)
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 3077)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Rek4) mRNA, complete
                         Similarity
                                                                                                                                              877
                                                                                                                                                                                                                                                     /product="cph-related receptor tyrosine kinase homolog"
/protein_id="AAC06273.1"
/protein_id="AAC06273.1"
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/db_xref="G: 1699722"
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LRDCNSIPTULGTCKETFNLYYMESDDDHGVRFLEHQFTK.1071AADESETQMDLGDR
ILKLNTEIREVGPVNKKGFYYAAFQDVGACVALVSVVVYFKKCPFTVKNLAMFPDTVPM
DSQSLVEVRGSCVNNSKEEDPPRMYCSTEGEWLVFIGACTCNAGYEERGFICACACRPG
FYKALDGVAKCTKCPPHSSTQEDGSMNCRCENNYFRAEKDPPSMACTRPPSAPRNVIS
NINETSYILDMSWPLDTGGRKDITFNIICKCGWNVRPCEPGSPNVRFLPRQLGLTNT
TVTVTDLLAHTNYTFEIDAINGVSELSSPERQFFAVSITINQAAPSPVMTIKKDRTSR
NSISLSWQEPEHBNGIILDYEKKYYEKQEQETSYTILLARGTNVTISSLKPDTTYVFQ
IRARTAAGYCTNSRKEEFENSPDSFSISGENSHVVMLAISGTAVAIIVLTVVTYTVLVGR
FCGYHKSKHSSDEKRLHFGNGHLRLPGLATTVDPHTYEDDFQAVHEFAKELDATNIAI
DKVVGAGEFGEWCGSTLKLPSKKEISYAIKTLKVGYTEKQRRDFLGEASINGOTHPN
IIRLEGVVTKSKPVMIVTEYMENGSLDSFLRKHDAQFTVIQLVGMLRGIASGMKYLSD
MGYVHADLAARNILINSNLVCKVSDFGLSRVLEDDPEAAYTTRGGKIFVRWTSBEATA
VERFFGSASTAGGGTULWETWEGSEDDFEARYTERGGKIFVRWTSBEATA
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norvegicus
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                                                                                                                                              ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="cardlomyocytes"
1. .3077
                                                                                                                                              LETQSKNGPVPV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Rattus norvegicus"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                           HTTGDWLNGMRTAHCKEIFTGVEYSSCDTIAKISTDDMKKVGVTVVGPQKKIISSIKA
                                                                                                                                                                                                                                         YRKFTSASDVWSYGIVLWEVMSYGERPYWEMSNQDVIKAVDEGYRLPLPMDCPAALYQ
                                                                                                                                                                                                                    LMLDCWQKDRNNRPKFEQIVSILDKLIRNPGSLKIITSAAARPSNLLLDQSNVDIATF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="Rek4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="neonatal"
/cell_type="cardiomyo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .3077
                         70.6%;
81.6%;
Score 61.4; DB 12;
Pred. No. 5.4e-10;
0; Mismatches 16;
                                                                                                                                            758 g
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TITLE
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                                                                         gaactgattccgcagccttccaatgaa 87
gaactgattccgcagccttccaatgaa
                                            ATGGATTGTCACCTCCATCCTCGTCCTGCTCGGCTGCTGCGTCCTCAGCTGCTCCGGA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAACTGAGTCCACAGCCTTCCAACGAA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M68513.1 GI:19911y
receptor tyrosine kinase.
receptor tyrosine kinase.
Minaculus (strain IRC x Swiss Webster) 11.5 day embryo embryo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 3197)

Sajjadi,F.G., Pasquale,E.B. and Subramani,S.

Identification of a new eph-related receptor tyrosine kinase gene from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor

New Biol. 3, 769-778 (1991)
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                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                          907
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 VTVTDLLAHTNYTFEIDAVNGVSELSSPPRQYAAVSITTNQAAPSPVMIKKDRTSRN
SISLSROEPEHPRGILLDYEVKYYQKOEQETSYTILARAGTNYTISSLKEPTTYVFOI
RARTAAGYGTYSKREFEETSPDSFSIGENSHYVMIAISAAVAIIVLTVYTYVLVGRF
CGYHKSKHSAEEKRLHFGNGHLKLPGLKTYVDHTYEDPTQAVHEFAKELDATNISID
KVVGAAEFGEYCSGRLKLPSKKEISVALKTLKYGYTEKORNDFLGEASINGODHPNI
IRLEGVYTKSKPEMIVTEYMENGSLDSFLKHDAQFTVFQLVGMLRGIASGMKYLSDM
GYVHRDLAARNILINSHLVCKVSDFGLSRVLEDDPEAAYTTRGGXIPIRMTSPEAMSY
GYVHRDLAARNILINSHLVCKVSDFGLSRVLEDDPEAAYTTRGGXIPIRMTSPEAMSY
GYNHRDLAARNILINSHLVCKVSDFGLSRVLEDDPEAAYTTRGGXIPIRMTSPEAMSY
GYNHRDLAARNILINSHLVCKVSDFGLSRVSQMSNQDVIRAVDERXRLPPPMDCPAALYQL
                                                                                                                                                                                                                                                                                                       ETQSKNGPVPV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISYPSHGWEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFT
LRDCNSIPLVLGTCKETFNLYYMESDDHGVKFREHQFTKIDTJADESETQMDLGDRI
LKLNTEIREGPVNKKGFYLAFQDVGACVALVSVRVYFKCPFTVKNLAMFPDTVFND
LKLNTEIREGFYLNSKKGFYLAFQDVGACVALVSVRVYFKCPFTVKNLAMFPDTVFND
SQSLVEVRGSCVNNSKKGFYLAFQDVGACVALVFIGKCTCNAGYEERGFICQACRPGF
YKASDGAAKCAKCPPHSSTQEDGSMNCRCENNYFRAEKDPSMACARPFSAPRNVISN
INETSVILDWSWPLDTGGRKDITFNIICKKCGWNVRQCEPCSPNVRFLPRQLGLTNTT
                                                                                                                                                                                                                                                                                                                                                    MLDCWQKDRNNRPKFEQIVSILDKLIRNPGSLKIITSAAARPSNLLLDQSNVDIATFH
TTGDWLNGMRTAHCKEIFTGVEYSSCDTIAKISTDDMKKVGVTVVGPQKKIISTIKAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="receptor tyrosine kinase"
/protein_id="AAA39521.1"
/db_xref="GI:199120"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="Mek4"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="IRC x Swiss Webster"
/db_xref="taxon:10090"
/dev_stage="11.5 day embryo"
/tlssue_type="embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="Mek4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
                                                                                                                                                                         70.6%;
                                                                                                                                            Score 61.4; DB 12;
Pred. No. 5.5e-10;
0; Mismatches 16;
                                                                                                                                                                                                                                                                                                     748
                                                                                                                                                 Indels
                                                                                                                                                                                              Length
                                                                                                                                                                                                   3197;
                                                                                                                                              0;
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AUTHORS
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* NOTE: This record contains 87 individual

* NOTE: This record contains 87 individual

* sequencing reads that have not been assembled into

* contigs. Runs of N are used to separate the reads

* and the order in which they appear is completely

* arbitrary. Low pass sequence sampling is useful for

* thentifying clones that may be gene-rich and allows

* overlap relationships among clones to be deduced.

* However, it should not be assumed that this clone

* will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (14-JAN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 53997) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 53997)
Waterston, R.H.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC021186
AC021186.1 GI:6693396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MO 63108,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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               8688
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5494
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       2: gap of unknown length
2: contig of 850 bp in length
2: gap of unknown length
3: gap of unknown length
5: contig of 439 bp in length
5: contig of 404 bp in length
6: gap of unknown length
7: contig of 842 bp in length
7: contig of 842 bp in length
7: gap of unknown length
8: contig of 446 bp in length
8: contig of 446 bp in length
8: contig of 470 bp in length
8: contig of 470 bp in length
8: contig of 6133 bp in length
6: contig of 133 bp in length
6: contig of 133 bp in length
6: gap of unknown length
6: contig of 133 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gap of unknown length
contig of 831 bp in length
gap of unknown length
contig of 470 bp in length
gap of unknown length
contig of 362 bp in length
gap of unknown length
gap of unknown length
contig of 427 bp in length
gap of unknown length
length
contig of 154 bp in length
length
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                                                                                                                                                                                                                                                                                                                                                                                                                      of 154 bp in length
unknown length
of 455 bp in length
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13758: 13768: 14181: 14191:

14651: 14661: 14986:

14996 :

of unknown length g of 187 bp in length of unknown length of unknown length g of 752 bp in length g of 596 bp in length of unknown length of wnknown length of of 922 bp in length of unknown length	of unknown length of withown length of unknown length of 461 bp in length of unknown length of 465 bp in length of unknown length of 475 bp in length of unknown length of unknown length of unknown length of unknown length of withown length of unknown length of 453 bp in length of unknown length of withown length of unknown length of f 338 bp in length of unknown length of s86 bp in length of unknown length of s86 bp in length
Query Match 33.3%; Score 29; DB 44; Length 53997; Best Local Similarity 63.8%; Pred. No. 24; Matches 44; Conservative 0; Mismatches 25; Indels 0; Gaps Qy 13 ctctccatcctcctcctcagctgctcttctcgacagcttcggggaactgattccg 72	33476 33485 gap of unknown length 33486 all46: contig of 661b pt in length 33487 33485 gap of unknown length 33487 33537 contig of 1076 bp in length 33537 gap of unknown length 33538 gap of unknown length 33543 gap of unknown length 33553 gap of unknown length 33554 gap of unknown length 33555 gap of unknown length 33555 gap of unknown length 33556 gap of unknown length 33557 gap of unknown length

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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
For further information about this sequence, including its location For further information about this sequence, visit our sequence of the sequence of
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Svirskas, R.R., Harris, N.L., Agbayani, A., Arcaina, T.T., Baxter, E.,
Blazej, R. G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E.,
Flanagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,
Kim, S.H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Mok, M.S.,
Moshrefi, M., Mixon, K., Pacleb, J.M., Park, S.,
Pfeiffer, B., Punch, E., Snir, E., Twomey, B., Wan, K.H., Whitelaw, K.R.,
Pfeiffer, B., Punch, E., Snir, E., Twomey, B., Wan, K.H., Whitelaw, K.R.,
Presidenting of Drosophila chromosome 2R, region 55C1-55C4
Unpublished (1997)
Unpublished (1997)
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Unsees I to 84551)
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1 (bases 1 to 84551)
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AC004295 AC003461 AC003462 AC003463 AC003824 AC003464 AC003825
AC003465 AC003466 AC003467 AC003468 AC003469 AC003470
AC004295.1 GI:3347818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and relationship to other sequences, please visit our sequence archive Web site (http://fruitfly.berkeley.edu/sequence/) or send email to drosophila@mhgc.lbl.gov. Library location: 22-88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (07-MAR 1998) Drosophila Genome Center, Lawrence Laboratory, MS 64-121, Berkeley, CA 94720, USA
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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19310 c 19295 g 23321 t
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/db_xref-"taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                      33.1%;
                                                                                                                                                                                                                                                                                                                                                                          Score 28.8;
Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                   Mismatches
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Direct Submission

Submitted (08-DEC-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Aug 26, 1999 this sequence version replaced gi:5763790.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                           HSRYR7CC1 119118 bp DNA PRI 12-DEC-1999
Human DNA sequence from clone XX-PRYR7CC1 on chromosome 22 Contains an STS, GSSs, genomic marker D22S928, tc and ca repeat polymorphisms and a putative CpG island, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was identified as CDM:10211270 by the submitter. For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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Submitted (10-DEC-1999) Celera Genomics, 45 West Gude Drive, Submitted, MD, USA
Rockville, MD, USA
                                                                                                                                                                                                                                                                                                                  Homo sapiens
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[ (bases 1 to 119118)
                                                                                                                                                                                                                                                                                                                                                           polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                HTG; ca repeat polymorphism; CpG island; D22S928;
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Similarity 65.68;
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/db_xref="taxon:7227"
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Pred. No. 31;
0; Mismatches 22;
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, *** SEQUENCING IN PROGRESS ***, in o
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This sequence was generated from part of bacterial clone contigs of

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C_elegans/wormpep IMPORTANT: This sequence is not the entire insert of clone XY-PXYR7CC1 It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPOT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              During sequence assembly data is compared from overlapping clumhere differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human chromosome 22, constructed by the Sanger Centre Chromosome Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr22
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                                                                                                                                       6501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Single clone region"
2719. .2726
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/db_xref="taxon:9606"
/chromosome="22"
                                                                                                                                                                            6178. .6472
/note="AluSq repeat: matches 1.
6473. .6500
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/note="12_copies 6 mer cccccg
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77. .504
                                                                                                                                                                                                                                       note="MER94 repeat: matches 47.
                                                                                                                                                                                                                                                                              'note="MIR repeat: matches 70. .172 of consensus"
                                                                                                                                                                                                                                                                                                      note="MIR repeat: matches 95. 3999. .6097
                                                                                                                                                                                                                                                                                                                                                                                         /note="AluSg repeat: matches 1. .307 of
1418. .4542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="Single clone region"
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                                                                   'note="MER21B repeat: matches 706. .789 of consensus"
                                                                                                                                                      note="MER94 repeat: matches 27.
                                                                                                                                                                                                                                                                                                                                                            'note="AluJo/FRAM repeat: matches 152. .276 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="Single clone region"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e="15 copies 26 mer 56 conserved" .488
                                                                                                                                                                                                                                                                                                                                                                                                                              "15 copies 2 mer tt 90 conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -"37 copies 2 mer cc 66 conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .2608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         214 copies 2 mer gg 55
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                              repeat: matches 18.
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                                                                                                                                                                                                                                                                                                                     .165 of consensus"
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                                                          /note="MLT1-INTERNAL repeat:
consensus"
19869. .20140
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/note="AluSq/x repeat: matches 9.8257. .8415
                                                                                                                                                                                       /note="AluSx repeat: 19069. .19100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="AluSq repeat: matches 1.
complement(15768. .16376)
/note="match: GSS: Em:AQ476535"
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8005. .8080
/note="MER2 repeat: matches 269. .343 of consensus"
                          /note="AluJo repeat: matches 18.
20218. .20385
                                                                                                                                                                                                                                                                                                                                                          /note="26 copies 2 mer aa 73 conserved" 17222. .17308 /note="Lz repeat: matches 2652. .2738 of 17452. .17487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10871. .11171
/note="AluJo repeat: matches 1.
11190. .11487
/note="AluSx repeat: matches 1.
11610. .11726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="AluSq repeat: matches 57. .311 of consensus"
10736. .10821
note="11MA10 repeat: matches 6045. .6135 of consensus"
/note="MLT1B repeat: matches 1.
                                                                                                                                               consensus
                                                                                                                                                                                                                                                 /note="AluY repeat: matches 1. .310 of consensus"
18508. .18616
/note="LIPA6 repeat: matches 6035. .6143 of consensus"
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10481. .10735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="AluJo repeat: matches 13. .300 of consensus"
9266. .9580
                                                                                                                                                                     note="MLT1-INTERNAL"
                                                                                                                                                                                                                                                                                                                                    'note="18 copies 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="MIR repeat: matches 73. .226 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="MLTIC repeat: matches 355.
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10270. .10480
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note="AluJo/FRAM repeat: matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e="L1PA10 repeat: matches 5476. .6165 of consensus"
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                                         .288 of consensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCCCTT 12858
                                                                                                                                   Direct Submission
Submitted (09-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Feb 2, 2000 this sequence version replaced g1:6693437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC017104 183776 bp DNA HTG 02-F HOMO Sapiens clone RP11-56215, WORKING DRAFT SEQUENCE,
2 (bases 1 to 183776) Waterston, R.H.
                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 183776)
Waterston, R. H.
                                                                 Center: Washington University Genome Sequencing Center Center code: WUGSC
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HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                   Unpublished
                                                                                                                                                                                                                                                                  The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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AC017104.3
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Feb 2, 2000 this sequence version replaced g1:6693437.
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/note="match: GSS: Em.AQ529159"
complement(24086...24604)
/note="match: GSS: Em:AQ569063"
24115...24201
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complement(24215 .24582)
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20685. .20736
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Chemistry: Dye-primer ET; 88% of reads
Chemistry: Dye-terminator Big Dye; 12% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 168893 bases at least Q40
Consensus quality: 174250 bases at least Q30
Consensus quality: 177018 bases at least Q20
Insert size: 183776; sum-of-contigs
Quality coverage: 3.77 in Q20 bases; sum-of-contigs
Quality coverage: 3.55 in Q20 bases; sum-of-contigs
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3630: contig of 2411 b
gap of unknown 1
5029: contig of 1399 b
gap of unknown 1
8124: contig of 3095 b
gap of unknown 1
9784: contig of 1660 b
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/organism="Homo sapiens"

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SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   requests: clonerequest@sanger.ac.uk
on Nov 29, 1999 this sequence version replaced gi:@468554
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
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                                                                                                                                                                                                            The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6
RP1-72EL7 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pleter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (29-NOV-1999) Sanger Centre, Hinxton, Cambridgeshire. CB10 1SA, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone
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1 (bases 1 to 90299)
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1 44968 c 44823 g 47139
      /clone_lib="RPCI-1"
7992. .8401
                                             /map="p24.1-25.3"
/clone="RP1-72E17"
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/db_xref="taxon:9606"
                                                                                      'chromosome="6"
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                                                                                                                                             Homo sapiens chromosome 19 clone CITB-H1_2329C7, SEQUENCE, 44 unordered pieces.
Eukaryota; Metazoa; Chordata; C
Eutheria; Primates; Catarrhini;
1 (bases 1 to 187701)
DOE Joint Genome Institute.
Sequencing of Human Chromosome
                                                                                    Homo sapiens
                                                                                                                AC010485.2 GI:6693194
HTG; HTGS_PHASE1; HTGS_DRAFT
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/note="match: 611636 ..11917
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80516. .81048
/note-"match: GSS: Em:AQ767778.
20192 c 20337 g 25131 t
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complement(41285. .
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complement(41270, .41845)
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complement(17175. 17672)
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complement(17272. 17672)
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complement(12136. .
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                                                               Vertebrata; Mammalia;
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2 (bases 1 to 187701)
DOE Joint Genome Institute.
Direct Submission
Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jan 14, 2000 this sequence version replaced gi:5882452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Joint Genome Institute
Center Code: JGI
Web Site: http://www.jgi.doe.gov
-----Summary Statistics
Consensus quality: 12926 bases at least Q40
Consensus quality: 142143 bases at least Q30
Consensus quality: 147093 bases at least Q20
Estimated insert size: 187701; sum-of-contigs estimation
Estimated insert size: 125880; sagarose-fp estimation
Ouality coverage: 8.86x in Q20 bases; sum-of-contigs estimation
Ouality coverage: 5.95x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 44 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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RESULT 14 AL138881 LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS	Qy 68 t1 Db 181214 To	Qy 8 91 Db 181274 GJ	Query Match Best Local (Matches 4)	BASE COUNT ORIGIN		FEATURES Source																					
AL138881 211385 b) HOMMO SAPIENS Chromo: PROGRESS ***, 50 und AL138881 AL138881.1 GI:6982 HTG; HTGS_PHASE1.	tccgcagccttc 80 GCCGCAGGATTC 181202	tcagctctccatcctcctc ACAGCTTCCCCTCTCCCTC	32.4 Similarity 61.6 5; Conservative	/chromoson /clone="c: 47607 a 47529 c	organism db_xref=	Location/Q 1, .187701	+ 124846 18770:	* 102398 12484!	83414 10239	69869 8341	* 60770 69868	* 59473 60769	* 56459 59472	* 54516 56458	* 52830 54515	* 50802 52829	* 48949 50801	* 47444 48948	* 45614 47443	* 44463 45613	* 43165 44462	* 41919 43164 *	39807 41918	* 38429 39806	* 36810 38428	* 35295 36809 *	* 34099 35294
p DNA some 6 clone RP11-52 ordered pieces.		ctccttctcagctgctctgttctcgs 	%; Score 28.2; DB 44; %; Pred. No. 50; 0; Mismatches 28;	ne="19" ITB-H1_2329C7" 45578 g 46667 t	"Homo sapiens" "taxon:9606"	ualifiers	contig of 62856	p or	tig of 18984	tig of 13545	ntig of	contig of 1297	contig	contig of 1943	gap of unknown ler	contig of 2028 bp	gap of unknown ler contig of 1853 bp	e contig of 1505 bp	contig of 1830 bp in	contig of 1151 bp	contig of 1298 bp	contig of 1246 bp	contig of 2112 bp	contig of 1378 bp	contig of 1619 bp	contig of 1515	gap of unknown ler contig of 1196 bp
HTG 05-FEB-2000 8H16, *** SEQUENCING IN		tctgttctcgacagcttcggggaactga 67	; Length 187701; ; Indels 0; Gaps	320 others			in length.	in length	in length	in length	n length th	length	length	length	n length -h	length	length	ler	length	length	length	n length -h	length	length	length	length	h length

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On Feb 16, 2000 this sequence version replaced 91:6912160.

MPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in
progress and the release of this data is based on the understanding
that the sequence may change as work continues. The sequence may
be contaminated with foreign sequence from E.coli, yeast, vector,
phage etc. Order of segments is not known; 800 n's separate
segments: Contig.ID: 00006 Length: 9572bp
Contig.ID: 00022 Length: 10:57bp
Contig.ID: 000021 Length: 9572bp
Contig.ID: 00051 Length: 9572bp
Contig.ID: 00051 Length: 9572bp
Contig.ID: 000151 Length: 9572bp
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Contig.ID: 000151 Length: 9572bp
Contig.ID: 00020 Length: 9572bp
Contig.ID: 000151 Length: 9572bp
Contig.ID: 000151 Length: 9572bp
Contig.ID: 00021 Length: 9572bp
Contig.ID: 000151 Length: 9572bp
Contig.ID: 000151 Length: 9572bp
Contig.ID: 000151 Length: 9572bp
Contig.ID: 00199 Length: 9572bp
Contig.ID: 00210 Length: 9572bp
Contig.ID: 00311 Length: 383bp
Contig.ID: 00311 Length: 383bp
Contig.ID: 00312 Length: 9572bp
Contig.ID: 00313 Length: 342bp
Contig.ID: 00314 Length: 3313bp
Contig.ID: 00472 Length: 1855bp
Contig.ID: 00473 Length: 1855bp
Contig.ID: 00493 Length: 1855bp
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Contig.ID: 00506 Length: 1859bp
Contig.ID: 005
Contig_ID: 00337 Length: 2333bp
Contig_ID: 00386 Length: 4205bp
Contig_ID: 00464 Length: 3133bp
Contig_ID: 00472 Length: 3133bp
Contig_ID: 00487 Length: 3603bp
Contig_ID: 00493 Length: 175bp
Contig_ID: 00499 Length: 175bp
Contig_ID: 00506 Length: 1159bp
Contig_ID: 00508 Length: 1159bp
Contig_ID: 00518 Length: 1319bp
Contig_ID: 00549 Length: 1319bp
Contig_ID: 00549 Length: 1338bp
Contig_ID: 00550 Length: 1338bp
Contig_ID: 00564 Length: 1338bp
Contig_ID: 00564 Length: 1338bp
Contig_ID: 00561 Length: 1392bp
Contig_ID: 00561 Length: 1342bp
Contig_ID: 00561 Length: 1442bp
Contig_ID: 00662 Length: 1455bp
Contig_ID: 00661 Length: 1455bp
Contig_ID: 00665 Length: 1455bp
Contig_ID: 00666 Length: 1455bp
Contig_ID: 00737 Length: 1455bp
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Contig_ID: 0074 Length: 1355bp
Contig_ID: 0074 Length: 1355bp
Contig_ID: 00766 Length: 1355bp
Contig_ID: 00876 Length: 2452bp
Contig_ID: 00876 Length: 2452bp
Contig_ID: 00876 Length: 2452bp
Contig_ID: 00955 Length: 2452bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 211385)
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258: gap of 1847: conti 217: gap of 2305s: conti 2561s: conti 2561s: gap of 413: gap of 52799: conti 32583: conti 32583: conti 33515: conti 5115: gap of 40220: conti 5010: gap of 5050: gap of 5050: gap of	### OF THE PROPERTY OF THE PRO	2: gap of 5: yap of 9: gap of 9: gap of 9: gap of 9: gap of 9: gap of 2: gap of 2: gap of 2: gap of 5: gap of 5: gap of	s availab 72: conti gap of 88: conti gap of 45: conti gap of 175: conti gap of 12: conti
# 1000 bp	of 3422 by 68 800 bp of 2333 bp 800 bp of 4205 bp of 1855 bp 6800 bp of 313 bp of 3603 bp of 1719 bp of 1451 bp of 1451 bp	800 b 800 b 800 b 800 b 800 b 800 b 1982 800 b 1982 800 b 1982 800 b	and the 800 bp 800 bp of 1016 b 800 bp 61 1557 b 900 bp 67 2972 b 800 bp 67 4358 b 6800 bp 67 4358 b 6
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2 (bases 1 to 307834)
DOE JOINT Genome Institute.
Direct Submission
Submitted (15-SEP-1999) Production Sequencing Facility,
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 307834)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                              Homo sapiens chromosome
SEQUENCE, 59 unordered p
AC010475
AC010475.2 GI:6693197
                                                                                                                      Unpublished
                                                                                                                                              Sequencing of Human Chromosome
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150920 157061: contig of 6142 bp in
157062 157861: gap of 800 bp
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/db_xref="taxon:9606"
/chromosome="6"
/clone="rp11-528H16"
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163529: gap of 800 bp

166583: contig of 3054 bp in 1

67383: gap of 800 bp

168838: contig of 1455 bp in 1

69638.
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Pred. No. 50;
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5 clone CITB-H1_2308B20, WORKING DRAFT
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  DOE Joint
94598, USP
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-----Summary Statistics
Consensus quality: 224141 bases at least Q40
Consensus quality: 249816 bases at least Q30
Consensus quality: 258890 bases at least Q20
Estimated insert size: 307834; sum-of-contigs estimation
Estimated insert size: 120000; pulse field gel estimation
Quality coverage: 15.47x in Q20 bases; pulse field gel estimation
Quality coverage: 6.03x in Q20 bases; sum-of-contigs estimation
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Query Match Best Local S Matches 48

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Search completed: May 15, 2000, 11:43:02 Job time: 18609 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

TITLE JOURNAL	REFERENCE AUTHORS	SOURCE ORGANISM	ACCESSION VERSION	LOCUS DEFINITION	RESULT 1 H38363		4 4 4 0 4 0						3 W (16 17	15		111	10		10			L	No.
Wilson,R. The WashU Unpublish	Eutheria 1 (base Hillier Holman, Parsons Trevask	human. Homo saj Eukaryoi	RECEPTOR H38363 H38363.1	H38363 YP50g04 IMAGE:1			23.8 36.1 23.8 36.1 23.8 36.1																							30 45.5 27.2 41.2	9 !	Score Match
Wilson,R. The WashU-Merck EST Project Unpublished (1995)	Eutheria; Primates; Cata: 1 (bases 1 to 435) Hillier, L. Clark, N. Du Holman, M., Hultman, M., K Parsons, J., Rifkin, L., R Parsons, J., Rifkin, L. R Trevaskis, E., Waterston, R	human. Homo sapiens Eukaryota; Metazoa;	R HEK PRECUR 1 GI:907862	435 rl Soares 90902 5' s			.1 536 .1 565 .1 733																								1	Length
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roject	heria; Primates; Catarrhini; Hominidae; (bases 1 to 435) Lier, Clark, N., Dubuque, T., Elliston, man, M., Hultman, M., Kucaba, T., Le, M., Le, "Sons, J., Rifkin, L., Rohlfing, T., Soares, waskis, E., Waterston, R., Williamson, A.	hordata: Crani	R (HUMAN);, mRI	mRNA ina N2b4HR Homo ar to gb:M8394:		ALIGNMENTS	AQ708302 N38130 AU077466	N80340 AQ655614	AV214670 H69538	AI003549 AA376236	H55902 AA038832	AI195110	AA720125	H17411	AQ522265 AQ656077	AV345313	A1652683	AI655503 AI655522	AQ718452 AW261950	AW261956	AQ572153	AA123801	AA0000559 AA762271	AA466804	AA726779	AQ338519 W30350	AA212205	AV080438	N87424 AU080921	AA586761 R62432	36	IB
	Homo. K., Hawkinnon,G., M., Tan,F	ata: Vertebrata: Mammalia:	NA sequence.	H38363 435 bp mRNA EST 16-AUG-1995 yp50g04.rl Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:190902 5' similar to gb:M83941 TYROSINE-PROTEIN KINASE			AQ708302 HS_5569_A N38130 19357 Lambd AU077466 AU077466	N80340 yz91h06.r1 AQ655614 Sheared D	AV214670 AV214670 H69538 yr89c05.s1	AI003549 a188a09.s AA376236 EST88631	H55902 yr02c08.s1 AA038832 m195g12.r	AUSSIUSS nDebUUISE AI195110 u160q06.x	AA720125 33318 Lam	H17411 ym40c11.s1	AQ522265 HS_5200_A AQ656077 Sheared D	AV345313 AV345313	A1652683 wb30e10.x	AI655503 ttl3e07.x	AQ718452 HS_5516_B AW261950 xg29c10.x	AW261956 xq29d10.x	AQ572153 HS_2108_B	AA123801 mp96d07.r	AA000659 mg26a04.r AA762271 vw60g01.r	AA466804 Vd90g11.r	AA726779 VU42f03.r	AQ338519 HS_3118_B W30350 mc25e10.r1	AA212205 mu80b06.r	AV080438 AV080438	N87424 L3865F Huma	AA586761 nn71c10.s R62432 yq52e11.s1	H38363 yp50q04.r1	Description
TITLE	SOURCE ORGANISM REFERENCE AITTHORS	ACCESSION VERSION KEYWORDS	AA586761/c LOCUS DEFINITION	RESULT 2	Qy 61 c	Oy 1 9 Db 154 G	Best Local Matches 6	Ouery Match	ORIGIN	BASE COUNT													FEATURES									COMMENT
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/tissum_type="retina"
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P http://www.ncbi.nlm.nih.gov/ncicgap.
IP cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Wilson RK
ton University School of Medicine
rest Park Parkway, Box 8501, St. Louis, MO 63108
4 286 1810
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estewatson.wustl.edu
Size: 2663
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Fax: 314 400 1012
Email: est@watson.wustl.edu
Insert Size: 2443
High qality sequence stops: 337 Source: IMAGE Consortium, LINL This
Clone is available royalty-free through LINL; contact the IMAGE
Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                      Unpublished (1995)
Unpublished (1995)
On May 9, 1995 this sequence version replaced
Contact: Wilson RK
Washington University School of Medicine
Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M. Parsons, J., Rikin, L., Rohlfing, T., Soares, M., Tan, F., Trevaskis, E., Waterston, R., Williamson, A., Wohldmann, P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 487)
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IMAGE:36023
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Contact: Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wilson, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome
Clone distribution: NCI-GAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
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/db_xref="taxon:9606"
/clone="IMAGE:1089330"
/clone=lib="NCI_CGAP_Larl"
/clone_type="larynx"
/tissue_type="larynx"
/lab_host="SOLR (kanamycin resistant)"
/note="SOLR (kanamycin resistant)"
/note="Olgan: larynx; Vector: Bluescript SK-; Site_1:
/note="Organ: larynx; Vector: Bluescript SK-; Site_1:
/note="SOLR (kanamycin resistant)"
/note="SolR 
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t: Robert Strausberg, Ph.D.
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/db_xref="taxon:9606"
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Pred. No. 0.55;
0; Mismatches
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                                                                                                                                                                                                                                                                           Department of Laboratory Medicine and University of Toronto Banting Institute, 100 College St., To
                                                                                                                                                                                                                                                                                                                              Unpublished (1996)
On May 9, 1995 this sequence version replaced g1:802248.
Contact: Liew CC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N87424 252 bp mRNA EST 01-APR-1996
L3865F Human fetal heart, Lambda ZAP Express Homo sapiens cDNA
clone L3865 5' similar to RECEPTOR PROTEIN-TYROSINE KINASE (HEK11),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38;
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                                                                                                                                                                                                                                Email: liewcc@utcc.utoronto
                                                                                                                                                                                                                                                              Tel: 4169788758
                                                                                                                                                                                                                                                                                                                                                                             cDNAs from fetal heart (1996)
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/lab_host="E. coli XLI-Blue"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site
XhoI; mRNA was purified from human fetal hearts (8 10
weeks). cDNA was synthesized using a XhoI-Oligo dr
adaptor-primer. EcoRI adaptors were ligated, followed
digestion with XhoI, for directional cloning into
                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="L3865"
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/clone="IMAGE:36023"
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Pred. No. 5
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Matches 34
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σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hashimoto,K., Kusuda,J., Toyoda,A., Tanuma,R., Ito,A., Hirata,M., Suzuki,Y., Sasaki,M. and Sugano,S.
Isolation of full-length cDNA clones from a mouse brain cDNA library made by oligo-capping method unpublished (1999)
On May 18, 1998 this sequence version replaced gi:3137227.
Contact: Katsuyuki Hashimoto
Division of Genetic Resources
National Institute of Infectious Diseases
National Institute of Infectious Diseases
National Institute of Infectious Diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AU080921 835 AU080921 Sugano mo 5', mRNA sequence.
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39; Conserv
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 835)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus
                                                                                     Similarity
                                                                                                                                            202
                                                                                                                                                                                                                                                                                                                                                                             l: khashi@nih.go.jp
http://www.nih.go.jp/yoken/genbank/.
Location/Qualifiers
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Sugano mouse
                                                                                                                                                                                                                                                                                                                        /strain="C57BL"
/db_xref="taxon:10090"
/clone="MNCb-6241"
                                                                                                                                                                                                                                                                              /dev_stage="adult"
/lab_host="TOP10"
                                                                                                                                                                                                                                                                                                    /sex="female"
                                                                                                                                                                                                                                                                                                             /clone_lib="Sugano mouse brain mncb"
                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
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                                                                         Score 26.2; D
Pred. No. 14;
0; Mismatches
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Pred. No. 11
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8 tactggattcaaaacaattcaaggggagctgggctggatctcttatccatcacatggg 66
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Unpublished (1999)
On Mar 10, 1998 thi
Contact: Chie Owa
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 341)
                                                                                                                                                                                                           mq73c06.r1 Stratagene mouse melanoma (#937312) Mus clone IMAGE:584362 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: genome-res@rtc.riken.go.jp
Thermostabilization and thermoactivation of thermolabile enzymes be trehalose and its application for the synthesis of full length cDN (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
Transcriptional sequencing: A method for DNA sequencing using RNA polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carninci, P., Shibata, K., Ozawa, Y., Akahira, S., Akiyama, J., Fukuda, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Eukaryota; Metazoa;
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AA125015.1 GI:1684192
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Tel: 81-298-36-9145
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1 (bases 1 to 254)
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/clone="2210414F24"
/clone_lib="Mus musculus stomach C57BL/6J adult"
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/strain="C57BL/6J"
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62 c 58 g
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                                                                                                                                                                                                                                                                                  AA212205 364 bp mRNA EST 31-JAN-199 mu80b06.rl Stratagene mouse melanoma (#937312) Mus musculus clone IMAGE:651827 5' similar to TR:61184951 G1184951 PHOSPHOTYROSINE INDEPENDENT LIGAND P62B FOR THE LCK SH2 DOMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66
                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 364)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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On Sep 12, 1996 this sequence version replaced Contact: Marra M/Mouse EST Project Washd-HHMI Mouse EST Project Washington University School of Medicinep 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                           Mus musculus
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Fax: 314 286 1810
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Oligo dT.
the K-1735
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Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCACGAG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTTTT 3'"
a 95 c 88 g 85 t
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/note="Organ: skin; Vector: pBluescript SK-; Site_1:
/note="Organ: skin; Vector: pBluescript SK-; Site_1:
ECORI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. From M2 cells, a highly metastatic derivative
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/clone_lib="Stratagene mouse melanoma (#937312)"
/tissue_type="melanoma"
/dev_stage="M2 cells"
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On May 18, 1995 this sequence version repi
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                         sequence.
AQ338519
AQ338519.1
                                                                                                                                                                                                                                                                                                                                                                                          AQ338519 394 bp DNA
HS 3118_B1_C10_MR CIT Approved Human Genomic Sperm
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401 Queen Anne Avenue
Tel: (206) 616-3618
Fax: (206) 616-3887
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:397675
                                                      Contact: Mahairas GG, Wallace JC,
High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                  Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                scanning the
                                                                                                                                                                  Sequence-tagged connectors: A sequence approach to mapping
                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Stratagene mouse melanoma (#937312)"
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Acad. Sci. U. S. A.
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                                      Seattle,
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genomic

survey

Homo

Mammalia;

Holzman, T., Adams, M.D.

and

12-JAN-1999 Library D

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                                                                                                                                                                                                                                                             Unpublished (1996)
on Apr 14, 1993 this sequence version replication warra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            w30350 416 bp mRNA EST 11-SEP-1996 mc25e10.rl Soares mouse p3NMF19.5 Mus musculus cDNA clone IMAGE:349578 5' similar to pIR:S33561 S33561 ref(2)P protein fruit fly; mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 416)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3118 row: F column: 19
Seq primer: M13 Reverse
Class: BAC ends
                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Location/Qualifiers
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39; Conservative
                                                                                                                    primer: ETPrimer
                                                                         quality sequence stop: 414.
Location/Qualifiers
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314 286 1810
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E-Coli DH10B"
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:349578"
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/clone_11b="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
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On May 5, 1995 this sequence version replation contact: Marra Myouse EST Project
Washu-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Ld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA726779 426 bp mRNA
AA726779 426 bp mRNA
vu42f03.r1 Barstead mouse myotubes MPLRB5 Mus musculus CDNA clone
IMAGE:1194077 5' similar to TR:013502 013502 PHOSPHOTYROSINE
INDEPENDENT LIGAND P62B FOR THE LCK SH2 DOMAIN B-CELL ISOFORM ;,
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1 (bases 1 to 426)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
AA726779
AA726779.1 GI:2744486
                                                                                                                                                   MGI:641173
                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This_clone is available royalty-free through LLNL;
                                                                                                                                                                                                                Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                            The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                             Waterston, R.
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                                                                                                                                                               IMAGE Consortium (info@image.llnl.gov) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse.
                                                                                                              primer: -28m13 rev2 ET from Amersham h quality sequence stop: 419.
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/db_xref="taxon:10090"
/clone="IMAGE:1194077"
/clone_lib="Barstead mouse myotubes MPLRB5"
                                                     /strain-"C3H"
                                                                   /organism⇔"Mus musculus
                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                              Louis, MO 63108
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AA103674/c
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                                                                                                                                                                                                                                                                                 Unpublished (1996)
on Nov 29, 1993 this sequence version replaced Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA103674 434 bp mRNA EST 29-OCT-19 mo40c10.rl Life Tech mouse embryo 15 5dpc 10667012 Mus musc cDNA clone IMAGE:556050 5' similar to TR:G1184951 G1184951 PHOSPHOTYROSSINE INDEPENDENT LIGAND P62B FOR THE LCK SH2 DOI
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Waterston,R.

The WashU-HHMI Mouse EST Project
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 434)
                                                                                                                                                                                                Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further:
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314 286 1810
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/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:556050"
/clone_lib="Life Tech mouse embryo 15
/tissue_type="embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cell_line="C2C12"
/lab_host="DH10B"
                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The WashU-HHMI Mouse EST Project Unpublished (1996)
On Jan 25, 1995 this sequence version repl Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project WashU-HMI Mouse EST Project WashU-HMI Mouse EST Project WashU-HMI Mouse EST Project Teles 314 286 1800
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Seq primer: -28m13 rev2 ET from Amersham
High quality sequence stop: 409.
Location/Qualifiers
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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a 108 c 120 g 105 t
/clone_lib="Soares mouse
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/clone="IMAGE:807908"
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/lab_host="DH10B"
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On Apr 14, 1993 this sequence version replaced g1:693679.
Contact: Marra MyMouse EST project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Marra M., Hillier L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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           Bonaldo
                                                                                                                                                                                      /organism-"Mus musculus"
/strain-"C57BL/6J"
/db_xref-"taxon:10090"
/clone-"IMAGE:424878"
                                                                                                                                                   /sex="unknown"
                                                                                                                                                                      /clone_lib="Soares mouse
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston, R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
On May 8, 1995 this sequence version replaced gi:801194.
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
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Email: mouseest@vatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.5dpc embryos (total RNA provided by Minoru Ko, Wayne State Univ., from 2 ]; double-stranded cDNA was ligated ECO RI adaptors (pharmacia), digested with Not I and cloned into the Not I and ECO RI Sites of the modified p773 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo. "

a. 133 c. 140 g. 94 t. 1 others
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from mammary gland tissue from a lactating female, and was then priwith a Not I - oligo(dT) primer. Double-stranded cDNI ligated to Eco RI adaptors (Pharmacia), digested with
                                                                                                                                                                                                  /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:1248240"
                                                                                                                           /clone_lib="Soares_mammary_gland_NMLMG"
/sex="female (lactating)"
/tissue_type="mammary gland"
                                                                                                             /lab_host="DH10B"
                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             505 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata; Craniata; Vertebrata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 25.8; D
Pred. No. 19;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA
                                                                                                                                                                                                                                                                                                                                     Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
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Mus.
                                                                                                                                                                                                                                                                                                                                                                                                     contact the
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cDNA was
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I and cloned into the Not I and Eco RI sites of the modified pTTT3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "ORIGIN

OURTY Match

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Ouery Match

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Oxide to the Not I and Eco RI sites of the modified pTTT3 vector. Library is normalized. Library and M. Fatima Bonaldo. "Oxide to the Notation of the Notati
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Minimum
Maximum
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No.
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OM nucleic -
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
      Pred. No. is the score greater to and is derived by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Issued_Patents_NA: *
1: /cgn2_6/ptodata/2
2: /cgn2_6/ptodata/3
3: /cgn2_6/ptodata/3
4: /cgn2_6/ptodata/3
6: /cgn2_6/ptodata/3
7: /cgn2_6/ptodata/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match
      is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, rived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-104-340-7
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Gapop 10.0 , Gapext 1.0
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
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/cgn2_6/ptodata/2/ina/5C_COMB.seq:*
/cgn2_6/ptodata/2/ina/6COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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      GenCore version (c) 1993 - 2000
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US-08-167-919A-9
US-08-715-106-9
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US-08-449-645A-12
US-08-702-367A-12
PCT-US95-04681-12
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US-08-649-645A-1
US-08-649-645A-1
US-08-623-64681-1
US-08-63-64681-1
US-08-64681-1
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Sequence 9, Appli
Sequence 15, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 102, Appl
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  Sequence
                       100,
                   1, Appli
6, Appli
14, Appli
14, Appli
17, Appli
17, Appli
17, Appli
18, Appli
19, Appli
114, Appli
144, Appli

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US-08-167-919A-9
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21.4	21.4	21.4	21.6	21.6	21.6		21.8	21.8	21.8						21.8		21.8
32.4	32.4	32.4	32.7	32.7	32.7	33.0	33.0	33.0	33.0	33.0	33.0	33.0	33.0	33.0	33.0	33.0	33.0
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US-08-860-882A-25	US-08-449-287-3	US-08-442-542-5	US-08-162-809-11	US-08-162-809-17	US-08-162-809-7	US-08-976-838-28	US-08-976-838-17	US-08-525-940-17	US-08-976-838-19	US-08-525-940-19	US-08-976-838-20	US-08-525-940-20	US-08-976-838-22	US-08-525-940-22	US-08-976-838-14	US-08-525-940-14	US-08-368-852-14
Sequence 25, Appl	Sequence 3, Appli	Sequence 5, Appli	Sequence 11, Appl	Sequence 17, Appl	Sequence 7, Appli	Sequence 28, Appl	•	•	Sequence 19, Appl	-	-	-	Sequence 22, Appl	-	Sequence 14, Appl	Sequence 14, Appl	•

ALIGNMENTS

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TELEFAX: (516) 742-4343
TELEFAX: (516) 742-4343
TELEFAX: (516) 742-4366
TELEFAX: (516) 742-4366
TELEFAX: 901 SANS UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHAPARTERS: 1 NO. 19:
                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,919A
FILING DATE: 18-APR-1994
CLASSIFICATION NUMBER: PK6841 (AU)
FILING DATE: 21-JUN-1991
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK9992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU92/00294
APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-JUN-1992
ATTONNEY/ACENT INFORMATION
NAME: D1G19110, Frank S.
REGISTRATION NUMBER: 31.346
REFERENCE/DOCKET NUMBER: 31.346
REFERENCE/DOCKET NUMBER: 31.346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 5674691
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Boyd, Anuser APPLICANT: Simpson, Richard J.
APPLICANT: Wicks, Ian
APPLICANT: Wicks, Ian
APPLICANT: Ward, Larry D.
APPLICANT: Wikinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
TITLE OF INVENTION: AND USE THEREOF
             SEQUENCE CHARACTERISTICS:
LENGTH: 3132 base pair
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City STATE: New York

    Application US/08167919A
    5674691

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; LOCATION:
US-08-167-919A-9
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Best Local S
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Patent No. 6020306
                                                                                       FILING DATE: 18-APR-1994
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-UN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION NUMBER: PK992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION NUMBER: PCT/AU92/00294
APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-UN-1992
ATTORNEY/AGENT INFORMATION
NAME: D1G19110, FTANK S.
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
08/167,919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
                                                                 REFERENCE/DOCKET NUMBER: 91
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
TITLE OF INVENTION: AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187
                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 18-APP
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 catggg 66
                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATGGG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08715106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Scully, Scott, Murphy & Presser
400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wicks, Ian
Ward, Larry D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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100..3048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Simpson,
                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Boyd, Andrew W.
                                                  (516) 742-4343
                                                                                                                                                                                                                                                                                                                                              18-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                                                                                                               US/08/715,106
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Pred. No. 1.5e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 3132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                  US-08-162-809-15
               Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5457048 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15,
                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 514
ATTORNEY_AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 91.815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 535-9001
                                                                                                                                                                                                                              TELEFAX: (619) 535-89.
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 3254 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Foreydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS
                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 GTCAATCTACTGGATTCAAAAACAATTCAAGGGGAGCTGGGCTGGATCTCTTATCCATCA 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: San Diego
STATE: California
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Local Similarity 100.0%;
les 66; Conservative C
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STRANDEDNESS: sing
TOPOLOGY: linear
             Local
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                                                                                                                NAME/KEY:
                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: UZIP: 92122
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                                                                                                   LOCATION:
62; Conserv
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4370 La Jolla Village Drive, Suite 700
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               90.38;
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             Pred. No. 4.4e-14;
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Pred. No. 1.5e-16;
; Mismatches 0;
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Matches

Conservative

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Mismatches

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US-08-449-645A-12
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GENERAL INFORMATION:
                                                                                                      Sequence 12, Application US/08702367A Patent No. 5981246
                                          GENERAL INFORMATION:
APPLICANT: FOX, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERSKE/POCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FOX, GARY M.
TITLE OF INVENTION: EPH-Like
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
              NUMBER OF SEQUENCES: 4
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CLASSIFICATION: 435
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LOCATION: 1...
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   ADDRESSEE:
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DEDNESS: single
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Amgen Patent Operations/RBW
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US-08-702-367A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                            STREET: 1840 CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 3162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Lik
TITLE OF INVENTION: Kinases
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                                                                     ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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CLASSIFICATION:
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CLASSIFICATION: 435
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                                                                                                                                      APPLICATION NUMBER:
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3162 base pairs
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69.7%;
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Pred. No. 0.00031;
0; Mismatches 20
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US-08-449-645A-16

; Sequence 16, Application US/08449645A

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US-08-449-645A-16
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; LOCATION: 1...
PCT-US95-04681-12
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Best Local S
Matches 46
                                                                   Query Match
Best Local (
                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                  TOPOLOGY: 11: MOLECULE TYPE: FEATURE:
                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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    288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 69.7 tes 46; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                    LENGIH: 4529 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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Thousand Oaks California
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1840 Dehavilland Drive
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Pred. No. 0.00031;
0; Mismatches 20;
                                                    Score 31.2; DB 4
Pred. No. 0.0041;
0; Mismatches 1
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US-08-702-367A-16
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US-08-702-367A-16
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NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 4529 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1
Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 16, Application PC/TUS9504681 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION NUMBER: PCT/US95/04681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,367A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY ACCESS.
                                                                                                                                                                                                                                                                                                        STREET: 104v CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: EPH-Lik
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Fox, Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288 CTGCTGGATTCTAAAGCACAACAAACAGAGTTGGAGTGGATTTCCTCCTCCACCCAATGGG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE PATENT PC-DOS/MS-SOFTWARE: PatentIn Pc10-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1005/MS-1
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b. 5981246
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1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                             E: Amgen Patent Operations/RBW
1840 Dehavilland Drive
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186..3182
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Pred. No. 0.0041;
0; Mismatches 18; Indels 0
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CLASSIFICATION:

A-287

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: Sequence 102, Application US/08469537A

: Patent No. 5843749
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; LOCATION: 186
PCT-US95-04681-16
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Best Local Similarity
Matches 42; Conserv
                                                                                                                                  APPLICATION NUMBER: USSN 08/406,247
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 08/144,992
FILING DATE: 28-OCT-1993
APPLICATION NUMBER: USSN 07/736,559
FILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Ph.D., Gail M
REGISTRATION NUMBER: 32,143
REFERENCE/POCKET NUMBER: REG 070C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
TELEPAX: 914-345-7721
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NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
                                         INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3906 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,537A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 4529 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Maisonpierre, et al.
TITLE OF INVENTION: EHK AND ROR TYROSINE
TITLE OF INVENTION: KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Tarrytown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Regeneron Pharmaceuticals, Inc. STREET: 777 Old Saw Mill River Road
                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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Pred. No. 0.0041;
0; Mismatches 18;
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; FEATURE: CI; NAME/KEY: CI; LOCATION: 47; US-08-469-537A-102;
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                                                                                              Matches
                                                                                                                            Query Match
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Best Local
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                     NAME: Torchia, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 920C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/4.
FILING DATE: 15-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb 1
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS,MS-DOS
                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/3
FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               722 AATGGG 727
                                                                                           7 Match 44.2%;
Local Similarity 65.2%;
les 43; Conservative
                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
61 catggg 66
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les 43; Conserv
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T: 460 Point San Bruno Blvd
South San Francisco
: California
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65.2%;
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                                                                                           Score 29.2; DB 2; Length 4165;
Pred. No. 0.023;
0; Mismatches 23; Indels 0
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PCT-US96-00419-6
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US-08-440-815-1
Sequence 6, Application PC/TUS9600419
GENERAL INFORMATION:
APPLICANT: Thomas Clossek, Axel Ullrich, Birgit
APPLICANT: Millauer
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: MDK1 SIGNAL TRANSDUCTION DISORDERS
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08440815 Patent No. 5798448
                                                                                                                                                                                                                                                                                                                                                 Matches
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APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 4165 bases
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (denentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/330128
FILING DATE: 27-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 92
TELECOMMUNICATION INFORMATION:
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NAME: Torchia, Timothy E
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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nilarity 65.2%;
Conservative (
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415/952-9881
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Pred. No. 0.023;
0; Mismatches 23;
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MOLECULE TYPE:
PCT-US96-00419-6
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TELEPHONE: (213) 489-1600
TELEPAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2323
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GENERAL INFORMATION:
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Best Local Similarity
Matches 30. Conserve
                                                                                                                                                                                                                                                                                                APPLICANT: Thomas Clossek, Axel Ullrich, Birgit APPLICANT: Millauer TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF TITLE OF INVENTION: MDK1 SIGNAL TRANSDUCTION DISORDERS NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                  COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NITNERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: bod Angeles CITY: LOS Angeles CHATE: California
                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Wazburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 20
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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   PRIOR APPLICATION DATA: PRIOR APPLICATION DATA:
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                                      APPLICATION NUMBER: FILING DATE: Januar CLASSIFICATION:
                                                                                                                                                                                                                                           STREET: 633 West | CITY: Los Angeles STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: Januar CLASSIFICATION:
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STRANDEDNESS: sing.
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                                                         January 3,
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January 3, 1995
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66.1%;
                                                         PCT/US96/00419
y 3, 1995
including application
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Pred. No. 0.14;
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Best Local S
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                                                                                  NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 4:
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REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 208
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEPA: (213) 955-0440
TELEX: 67-3510
                                                                       INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Thomas Ciossek, Axel Ullrich, Birgit
APPLICANT: Millauer
TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: MDK1 SIGNAL TRANSDUCTION DISORDERS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                             SEQUENCE CHARACTERISTICS:
LENGTH: 4304
                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: Wordberfect (Version 5.1)
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    336 TACTGGACTCGAAAGCACAACAAACAGAATTGGAATGGATTTCCTCTCCACCCAGTGGG 394
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: Januar CLASSIFICATION:
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nes 39; Conserv
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STRANDEDNESS: singl
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STRANDEDNESS:
                 nucleic acid
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linear
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Y 3, 1995
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; MOLECULE TYPE:
PCT-US96-00419-1
Search completed: May 15, 2000, 12:05:06 Job time: 4425 sec
                                                                                     Query Match 40.9
Best Local Similarity 66.1
Matches 39; Conservative
                                              nucleic
                                                                                                  40.9%;
                                                                                      Score 27; DB 6
Pred. No. 0.16;
0; Mismatches
                                                                                                           DB 6;
                                                                                        20;
                                                                                                           Length 4304;
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                                                                                       Gaps
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Result
No.
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Maximum DB seq
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Listing first 45 summaries
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Perfect score:
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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34
nucleic search, using sw model
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length: 1000000
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Match
N_Geneseq_36:*
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Gapop 10.0 , Gapext 1.0
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66
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Length
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V70208
T14547
N90338
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T03100
T58840_2
T58840_3
Q60056

N80105

T99064

X01386

X01386

X01385

X01384

X01383

V19910

X20554

Q12399
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V58192
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T18893
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Q90659
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    Rat receptor tyros
Rat REK7 CDNA. AL-
Mouse developmenta
Mouse developmenta
Mouse developmenta
Mouse bak receptor
Rouse osteoblast-s
EPH-like receptor
EPH-like receptor
Protein tyrosine-k
Continuation (3 of
Continuation (4 of
Mus musculus cerbe
Rat receptor tyros
Cytotactin gene. C
Sequence of human
scFv-pp coding sequente protein
Human secreted pro
Human pro-protein
Polymphocyte prote
T-lymphocyte prote
Human pro-protein
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Embryonic stem cel
EPH-like receptor
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%	PF RG		RESULT Q34513 ID Q4513 AC Q DT Q DT Q DT Q DT Q PT Q ET T S	00000
Claim 6; Fig This sequence expressed in 1 tumours of hu and the epith (TK) and/or i production and analogues have cellular resp Sequence 31	19-JUN-1992; AU 21-JUN-1991; AU 12-DEC-1991; AU (HALL-) HALL IN BOYD AD, Simps WPI; 93-036373, P-PSDB; R31466. Receptor-type t III-A4 - is EPH Proteins in mod therapy etc.	misc_feature mat_peptide mat_peptide mat_peptide WO9300425-A. 07-JAN-1993.	OLT 1 513 Q34513 stan Q34513; 24-MAY-1993 HEK coding Primer; exp eph/elk-lik Lila-1; JM; TK; ligand; Synthetic. Key 5'utr cds 3'utr signal_pept	2000 444 444 600 600 600 600 600 600 600
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guence encodes human sed in both pre-B cells of human origin, eg epithelial tumour H didor its ligands are ion and/or function of the save activity in the responses such as the save as the save as the save activity in t	991; AU-006841. 991; AU-006841. 991; AU-009992. HALL INST MEDIC Simpson R, W 036373/04. R31466type tyrosine is EpH-ELK-lik in modulating etc.		dard; (fi sequeressins, ki.e; ki.e; ki.epitt.B;ce	32.7 32.7 32.7 32.7 32.7 32.7
58pp; En codes hubcodes hubcod	41 92 92 ne ne 1ii	/*tag= d 1/3: 1/3: 1/4: /*tag= e /note= "p 1:60 .216 /*tag= "p 2617 .26 /*tag= g /note= "p	DNA; 3132 irst entry) nnce. on vector; halial; He helial; He illular res Location/Q /*tag= a 100. 3051 /*tag= b 3/*tag= b 3/*tag= c /*tag= c	2187 2187 2187 2187 2394 2395 3105 3105 3751 3776 4049
mglisuman cell, eg ur He are ion cas sas sas sas sas sas sas sas sas sas	CAL R Ward kina ke kina	d 1795 e e "Pot 15 16 "Pur 2679 "Pur	3132 Bp htry) tor; ex tor; ex tor; HeLa; l; HeLa; l; HeLa; l; Tespon c respon c respon c respon c 13051 3051 3051 3051 3051	444444444
sh. eph/elk-like kina ls and T cell line This recepto useful as agents of pre-B, B and T transducing signal growth and/or diff h; 711 C; 75	ES WALTER & ELIZA LD, Wicks I, Wi se reactive with mase, useful for B, B and T cell f	ential transmembrane ified HEK protein #1"	P. xtracellular domain; cell; T; tunour; lym; receptor-type; thym nse; growth; differen	Q22146 V20546 X15186 Q22143 Q22143 Q12397 T07308 T84528 Q82461 Q90655 Q90655 Q90657
se (HEK). HEK is and in a number of LKG3, Lila-1 and JM, r-type thymidine kinase in modulation of the cells. The TK and its or in stimulating erentiation. 9 G; 774 T;	lkinson D; monoclonal antibody phosphorylating unction, in cancer	region"	human; HEK; lymphoid; LK63; hymiddne kinase; rentiation; ss.	Complete human HGF Human recombinant Nucleic acid encod Human HGF gene par Human hepatcocyte g Receptor tyrosine Mouse Nuk tyrosine Human embryonal ki Eph-related PTK Ce Eph-related PTK Ce

Ouery Match 100.0%; Score 66; DB 1; Best Local Similarity 100.0%; Pred. No. 2.1e-16; Matches 66; Conservative 0; Mismatches 0;

Length 3132; ; ; Indels

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Best Local 9
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08-JUN-1995; U10140.
07-SEP-1994; U5-162809.
03-DEC-1993; US-162809.
(LJOL-) LA JOLLA CANCER RES
PASGUALE EB. Sajjadi FG;
WPI: 95-215256/28.
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Disclosure; Page 85-89; 129pp; English.

Probes derived from the EPH-related PTKs Cek4 (Q90659) and Cek5 (Q90660) were used to isolate novel cDNA clones (Q90652-58, Q90661-62) from chicken embryo and embryonic brain libraries.

Cek4 is highly expressed in the chicken developing brain and embryonic tissues, as well as in the adult brain and retina.

Sequence 3254 BP; 926 A; 737 C; 796 G; 795 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eph-related PTK Cek4. Cek4; Eph; protein ty
                            WO9528484-A1.
26-OCT-1995.
14-APR-1995; U04681.
15-APR-1994; US-229509.
                                                                                                                                       T02947;
16-APR-1996 (first entry)
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                                                                                          Key
                                                                                                                      EPH-like receptor protein tyrosine kinase | EPH-like receptor protein tyrosine kinase;
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                                                                                                    Homo
(AMGE-) AMGEN INC.
Fox GM, Jing S, Welcher AA;
WPI; 95-373799/48.
                                                                                                              human eph-like
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176 CATGGG
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                                                                                                             kinase;
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                                                                                         Location/Qualifiers
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93.9%;
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                                                                                                            therapy;
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Pred. No. 6.3e-14;
0; Mismatches 4
                                                                                                             diagnosis;
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                                                                                                             vector; antibody;
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reconstitution and therapeutically to modulate receptor activation or prodn.

recons. (702946-49) coding for 4 novel human EPH-like receptor protein consecutively, coding kinases, HEK5, HEK7, HEK8 and HEK11 (R85089-92), respectively, cover isolated from a human foetal brain CDNA library using a directed CC PCR approach with primers (see T02960-61) based on conserved regions of creceptor PTKs and EPH-like receptor PTKs. HEK5, HEK7 and HEK8 show CC extensive homology to the catalytic domain of chicken EPH-like receptors. The isolated cDNAs are used for prodn. of creceptors CeK5, Cek7 and Cek8. HEK11 shows no homology to any known CC recombinant HEKS and chimeric receptors, in hybridisation assays, and CC to detect abnormalities in HEK receptor genes.

SQ Sequence 3162 BP; 921 A; 667 C; 775 G; 799 T;
                                           INA encoding embryonic stem cell kinase, receptor tyrosine kinase -

"for production of modulators and antibodies, useful to treat

"mucositis and other disorders involving epithelium

"Claim 4; Page 48-54; 98pp; English.

"A isolated nucleic acid molecule (172320) codes for novel mouse

embryonic stem cell kinase (Esk), a receptor tyrosine kinase that

"C belongs to the Eph subfamily. To isolate the molecule, RNA from

"C using primers (see also T72321-24) based on conserved Eph

"Sequences. A labelled probe from an isolated clone was used to

screen a mouse liver cDNA library, identifying a single clone that

Included the complete coding region of Esk. The gene for murine

Esk is located on bands B1 and B2 of chromosome 6. Esk nucleic

acids can be used to produce recombinant Esk polypeptides, develop

probes, and as sense and antisense molecules for diagnosis or
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Best Local S
Matches 46
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New nucleic acid encoding EPH-like receptor tyrosine kinase(s) and related vectors, host cells, proteins, antibodies etc., us diagnostically and therapeutically to modulate receptor activa
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20-DEC-1996; AU0826.
22-DEC-1995; AU-007277
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46; Conser
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9: Pred. No. 0.00
0; Mismatches
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receptor tyrosine kinase; mucositis;
rion; gene therapy; diagnosis; ss.
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Matches 43
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Claim 1; Page 66-71; 133pp; English.

CONAS (T02946-49) coding for 4 novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7, HEK8 and HEK11 (R85089-92), respectively, were isolated from a human foetal brain cDNA library using a directed PCR approach with primers (see T02960-61) based on conserved regions of receptor PTKs and EPH-like receptor PTKs. HEK5, HEK7 and HEK8 show extensive homology to the catalytic domain of chicken EPH-like receptors Cek5, Cek7 and Cek8. HEK11 shows no homology to any known EPH-like receptor. The isolated cDNAs are used for prodn. of recombinant HEKS and chimeric receptors, in hybridisation assays, and
                    11-FEB-1999 (first entry)
Rat receptor tyrosine kinase Ehk-1 encoding DNA.
Receptor tyrosine kinase; Ror-1; Ror-2; Ehk-1; E
neurotrophin activity; trkB; proto-oncogene; tyr
binding protein; BDNF; NT-3; diagnosis; ss.
                                                                                               V70207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid encoding EPH-like receptor tyrosine kinase(s) and related vectors, host cells, proteins, antibodies etc., used diagnostically and therapeutically to modulate receptor activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AMGE-) AMGEN INC.
Fox GM, Jing S, Welcher
WPI; 95-373799/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPH-like receptor protein tyrosine kinase HEK11 cDNA EPH-like receptor protein tyrosine kinase; PTK; HEK11 human eph-like kinase; therapy; diagnosis; antibody;
           Rattus sp
                                                                                                                                                                                                                                                                                                     to detect abnormalities in HEK receptor genes. Sequence 4529 BP; 1449 A; 834 C; 1000 G;
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42; Conserv
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US-229509.
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Pred. No. 0.00
0; Mismatches
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Pred. No. 0.0044;
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                                    tyrosine
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kinase rec
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                                    receptor;
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Best Local :
                                                                                                                                                                                                                                                                                                                             09-MAY-1996.
26-OCT-1995; U14016.
27-OCT-1994; US-330128.
07-JUN-1995; US-486449.
(GETH) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins
Claim 5; Fig 22; 194pp; English.
Claim 5; Fig 22; 194pp; English.
The present invention describes nucleic acid molecules for ror-1, enk-1 and ehk-2. Also described are the corresponding prot Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor tyrosine kinases. The present sequence encodes rat Ehk-1; tyrosine kinases. The present sequence encodes rat Ehk-1; 1097 A; 876 C; 990 G; 943 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US5843749-A.
01-DEC-1998.
06-JUN-1995;
17-MAR-1995;
         angiogenesis-related conditions.

Example 1; Page 47-49; 75pp; English.

A CDNA clone (T18893) codes for rat REK7 (R97853), an eph-related tyrosine kinase receptor, for which AL-1 (see also w97854) is a tyrosine kinase receptor, for which AL-1 (see captor tyrosine kinase ligand. It was isolated using degenerate receptor tyrosine kinase primers (T18894-96) to amplify cDNAs of an adult mouse hippocampal CDNA library. A PCR fragment was used as a probe to isolate the full-length REK7 cDNA from a rat hippocampal CDNA library. An extraction of the companion of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REK7; eph-related tyrosine kinase receptor; AL-1; ligand; neurotrophic factor; neuropathy; angiogenesis; therapy; or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T18893 standard;
T18893;
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WPI; 99-044584/04.
P-PSDB; W83147.
                                                                                                                                                                                                             AL-1 neurotrophic factor, an eph-tyrosine kinase ligand treatment and diagnosis of neuronal disorders and
                                                                                                                                                                                                                                                               P-PSDB; R97853
                                                                                                                                                                                                                                                                                        Caras IW, Winslow JW;
WPI; 96-239448/24.
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06-JUN-1995; US-469537.
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43; Conser
  fusion was used to screen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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541. .711
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712. .3324
/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       476. .3493
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Pred. No. 0.03
0; Mismatches
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336 TACTGGACTCGAAAGCAACAAACAGAATTGGAATGGATTTCCTCTCCACCCAGTGGG

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(PLAC) MAX PLANCK GES FI
(SUGE) SUGEN INC.
Clossek T, Millauer B,
WPI; 96-333988/33.
                                                         Example 1; Page 115-116; 128pp; English.

Example 1; Page 115-116; 128pp; English.

EDNA cloning using adult mouse brains and MDK1 T2 (T32962), that coded for truncated versions (W03422 and W03423, respectively) of the novel mouse developmental kinase 1 (MDK1) (see also T32960), a new member of the eck/eph family of receptor tyrosine kinases.

MDK T1 and T2 each possess the entire ectodomain, the transmembrane domain and part of the juxtamembrane region of MDK1 (see also W03421), but lack the catalytic tyrosine kinase domain. They may have a modulatory function. The cDNA clones can be used to produce MDK1 T1 and T2, which are useful for screening potential agents for treatment of diseases characterised by abnormal signal transduction. Sequence 2323 BP; 680 A; 497 C; 609 G; 537 T;
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11-JUL-1996.
03-JAN-1996; U00419.
03-JAN-1995; US-368776.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse developmental kinase 1 MDK1 T2 comouse developmental kinase 1; MDK1 T2; RTK; signal transduction; probe; diagno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     expression of REK7-binding activity. Primers based on isolated ligands were used to amplify human breast carcinoma BT20 cell cDNA, and an amplified fragment was used to screen a human foetal brain cDNA library, leading to the isolation of AL-1 cDNA (T18897). Sequence 4165 BP; 1157 A; 907 C; 1035 G; 1066 T;
                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                            mat_peptide
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/note= "divergent sequence
splicing"
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              40.9%;
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Matches 39
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03-JAN-1996; U00419.

03-JAN-1995; US-368776.

(PLAC) MAX PLANCK GES F

(SUGE-) SUGEN INC.

Clossek T, Millauer B,
                                                                                                                                                                                                                                                                                  Example 1; Page 111-12; 128pp; English.

Example 1; Page 111-12; 128pp; English.

CDNA cloning using adult mouse brains and MDK1 T2 (T32962), that identified 2 clones, MDK1 T1 (T32961) and MDK1 T2 (T32962), that coded for truncated versions (M03422 and M03423; respectively) of the novel mouse developmental kinase 1 (MDK1) (see also T32960), a new member of the eck/eph family of receptor tyrosine kinases.

MDK T1 and T2 each possess the entire ectodomain, the transmembrane domain and part of the juxtamembrane region of MDK1 (see also W03421), but lack the catalytic tyrosine kinase domain. They may have a modulatory function. The cDNA clones can be used to produce MDK1

T1 and T2, which are useful for screening potential agents for treatment of diseases characterised by abnormal signal transduction. Sequence 2901 BP; 890 A; 578 C; 650 G; 783 T;
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Mouse developmental kinase 1; MDK1 T1; receptor tyrosine kinase;
RTK; signal transduction; probe; diagnosis; gene therapy;
neurodegeneration; neuroproliferation; cancer; ss.
           Mouse developmental kinase 1; MDK1; rec
Mouse developmental kinase 1; MDK1; rec
signal transduction; probe; diagnosis;
neurodegeneration; neuroproliferation;
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                                                                                               standard;
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0; Mismatches
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                                      cDNA. ; MDK1; receptor tyrosine
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A cDNA clone (T32960) codes for mouse developmental kinase 1 (MDK1)

( W03421), a new member of the eck/eph family of receptor tyrosine

kinases (RTKs). To isolate the clone, cDNA from mouse embryos was

subjected to PCR amplification with primers based on conserved

motifs (see also W03426-27) of RTKs. An amplified fragment was used

to screen an 11.5-day-old mouse embryo and an adult mouse brain cDNA

library to obtain the MDK1 clone. 4 Sequence variants (see also

T32961-62 and W03422-25) of MDK1 were also identified. MDK1 nucleic

acids can be used for the recombinant prodn. of MDK1, as probes to

detect MDK1, and for the gene therapy of diseases involving

abnormalities in signal transduction, such as neurodegenerative and

neuroproliferative disorders and cancer.

Sequence 4304 BP; 1297 A; 875 C; 1043 G; 1089 T;
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Best Local S
Matches 39
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03-JAN-1996; U00419.
03-JAN-1995; US-368776.
(PLAC) MAX PLANCK GES F
(SUGE-) SUGEN INC.
Clossek T, Millauer B,
  US5814479-A.
29-SEP-1998.
11-JUN-1996;
04-JAN-1994;
                                                                                                                                                                                                                            25-NOV-1998 (first entry)
Mouse Bsk receptor-like tyrosine kinase cDNA clone.
Mouse; Bsk; receptor-like tyrosine kinase; brain; diagnosis; neurodegenerative disease; limbic system neuron regeneration; chromosomal abnormality; degenerative growth; development disviral infection; bacterial infection; Alzheimer's disease; epschizophrenia; stroke; cerebral ischaemia; ds.
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39; Conser
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  673789.
US-177812.
                                                                                 /product= "Bsk"
/note= "record
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                                                                                                                                                                Location/Qualifiers
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3568. .3573
/*tag= e
3627. .4304
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317. .:
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/note= "alternative
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233. .3229
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Pred. No. 0.27
0; Mismatches
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ies in
                                                                                             tyrosine kinase'
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0.27;
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                                                                                                                                                                                                                                                                                                                               diagnosis; neoplasm;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence encodes mouse Bsk, which is a receptor-like tyrosine kinase. The nucleic acid sequence encoding Bsk can be used in Bsk nucleic acid probes, which can be used in detecting alterations in the level of Bsk messenger-RNA (mRNA) in biological samples isolated from a mammal afflicted with a disease, such as neurodegenerative diseases or disorders and neoplasms. The nucleic acid sequence can also be delivered into the limbic system of patients with limbic system neurodegenerative disease, disorder or injury, to promote or enhance limbic system neuron regeneration or growth. Such neurodegenerative disease include, chromosomal abnormalities, degenerative growth and development disorders, viral infections, bacterial infections, brain schizophrenia, or stroke and cerebral ischaemia.

Sequence 4322 BP; 1260 A; 887 C; 1055 G; 1120 T;
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Best Loc
Matches
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(SCHU/) SCHULZ N T.
(WOUD/) WOUDE G F V.
(ZHOU/) ZHOU R.
(ZHOU/) ZHOU R.
                                                                                                                                                                                           EP-614974-A.
14-SEP-1994.
28-FEB-1994;
10-MAR-1993;
                                                                                                                                                                                                                                                                             Mus musculus.
Key
cds
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071303
071303;
           Claim 2; Page 8-11; 18pp; English.

Two cDNA libraries were prepared, one from murine osteoblast-like cell line MC3T3-E1 and the other from mouse hepatic tissues. Doubl stranded fragments of 300 bp were obtained using a random extensic primer and were blunt-ended. The ds linker ATOS-1/2 was ligated to the MC3T3-E1 cDNA and the ds linker ATOS-4/5 was ligated to liver
                                                                                                                                                                                                                                                                                                                     Mouse osteoblast-specific osteoblast-specific factor bone metabolic disease; di
                                                                                                        New osteoblast specific factor control factor in bone formation
                                                                                                                                                   (FARH ) HOECHST JAPAN LTD.
Amann E, Kawai S, Kikuno
WPI; 94-281204/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid sequence encoding protein - used in Bsk nucleic acid probes, used in detecting alterations in level of Bsk messenger-RNA in biological samples isolated from mammal afflicted
                                                                                               metabolic
                                                                                                                                                                                                                                                                                                                                                             11-APR-1995
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                                                                                                                                                                                                                                                /product= OSF-6
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                                                                                                                                                                                                                                                                                                                                  factor;
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                                                                                                         c factor -6 - active formation, used for
                                                                                                                                                                                                                                                                                                                   diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                        mRNA;
                                                                                                                                                                                                                                                                                                                               factor-6;
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Pred. No. 0.67
0; Mismatches
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0.67;
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was performed

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Proof.

Proof.

Scalaim 1; Page 41-45; 133pp; English.

CC cDNAs (702946-49) coding for 4 novel human EPH-like receptor protein CC cDNAs (702946-44) coding for 4 novel human EPH-like receptor protein CC tyrosine kinases, HEK7, HEK8 and HEK11 (R85089-92), respectively, comercial expression of the common common
                                                                                                                                                                                                                                                                                                                                         RESULT
T02948
ID T0
AC T0
DT 16
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                                                                                                                                                    밁
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Best Local S
Matches 37
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Best Local S
Matches 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fox GM,
WPI; 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Q71304) or ATOS-4 (Q71305), respectively. DNA specific for MC3TT-E1 was obtained by subtraction of sequences also found in liver library, then amplification with ATOS-1. This was a first step in the cloning procedure for isolating a MC3T3-E1 specific clone, coding for OSF-6 (see Q71303).

Sequence 2005 BP; 485 A; 534 C; 552 G; 434 T;
T02948 standard; cDNA;
T02948;
16-APR-1996 (first ent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding EPH-like receptor tyrosine kinase(s) and related vectors, host cells, proteins, antibodies etc., used diagnostically and therapeutically to modulate receptor activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPH-like receptor protein tyrosine kinase HEK5 cDNA EPH-like receptor protein tyrosine kinase; PTK; HEK human eph-like kinase; therapy; diagnosis; antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
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Fox GM, Jing S, Welcher
WPI; 95-373799/48.
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15-APR-1994; US-229509.
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                                                                                                                                                                                                                               Similarity 61.
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1. .2913
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61.7%;
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0; Mismatches
                                                                                                                                                                                                                                 Score 23.2; DB Pred. No. 7.3; 0; Mismatches
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Best Loc
Matches
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Claim 1; Page 57-62; 133pp; English.

CONNS (702946-49) coding for 4 novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7, HEK8 and HEK1 (R85089-92), respectively were isolated from a human foetal brain cDNA library using a directed PCR approach with primers (see 702960-61) based on conserved regions creceptor PTKs and EPH-like receptor PTKs. HEK5, HEK7 and HEK8 show extensive homology to the catalytic domain of chicken EPH-like receptors. The isolated cDNAs are used for prodn. of recombinant HEKS and chimeric receptors, in hybridisation assays, and
                                                                                                                                                                                                                                                     12-OCT-1995.
04-APR-1995;
04-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9528484-A1.
26-OCT-1995.
14-APR-1995; U
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Claim 1;
Agonist antibodies which activate specific protein tagonist antibodies which activate specific proteins of kina domain and Ig constant domain, useful for studying, modulation of, cell growth and differentiation Disclosure; Page 88-92; 125pp; English.

DNA probes based on protein tyrosine-kinase (pTK) se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo
Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein tyrosine-kinase | Protein tyrosine-kinase; differentiation; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid encoding and related vectors, host
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WPI; 95
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04-APR-1994; US-222616.
(GETH ) GENENTECH INC.
Bennett BD, Goeddel D,
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WPI; 95-366160/47.
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Y14271 Gallus gall
AL138846 Homo sapi
U21955 Rattus norv
X79084 M.musculus
U21954 Rattus norv
U58332 Mus musculus
U21954 Rattus norv
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AC009491 Homo sapi
AC009496 Homo sapi
AC009497 Senopus l
X6518 M.musculus
S57168 Sek-Eph-rel
AC015510 Homo sapi
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U73757 Mus musculu
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M68513 Mouse ephr

U69278 Rattus norv

L36644 Homo sapien

X95425 H sapiens m

U03910 Gallus gall

U72207 Mus musculu

AL035703 Human DNA

L36642 Homo sapien

AL121966 Homo sapi

AC015609 Homo sapi

AC021955 Homo sapi
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Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3132)
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ISYPSHGWEETSGVDEHYTPIRTYQVCNYMDHSQNNWLETNWYPRNSAQKIYVELKFT
LRDCNSIPLVLGTCKETFNLYYMESDDDHGVKREHQFTKIDTIAADESTTQMDLGDR
ILKLNTEIREVGPYNKKGFYLAFODVGACVAL/SVRYVFKKCPBTYKNLAMFDTVPM
DSQSLVEVRGSCVNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQACRPG
FYKALDGNMKCAKCPHSSTQEDGSMNCRCENNYIKQCEPCSSNVRFLPROFCLTNT
TYTVTDLLAHTNYTFEIDAVNGVSELSSPRQFGAVSITTNQAAPSPVLTIKKORTSR
NSISLSWGEPEHPNGILDVGKKUVYEKGEGETSYTILARAGTNYTISSLKEPDTIYVLQ
IRARTAAGYGTNSKREFETSPDSFSISGESQVVMIAISSAAVAILLITVVIYULIGR
FCGYKSKHGADEKRLHFGNGHLKLPGLRTYDDHTYEDDTQAVHEFAKELDATNISID
KVVGACEFGEVCSGRLKLPSKEISVALKTLKVGYTEKGATTROGLGEASIMGQPDHPNI
IRLEGVYTKSKPMIVTEYMENGSLDSFLRKDATVICHGMLRGIASGMKYLSDM
GYVHRDLAARNILTINSMLVCKVSDFGLSRVLEDDPEAAYTTRGKLPIFWTSPBAIAY
RKFTSASDVMSYGIVLMEWMSYGERFYWEMSNQDVIKAVDEGYRLPPMDCPAALYQL
MLDCWGKDRNNRPKFEQIVSILDKLIRDFGSRVLEDDPEAAYTTRGKLPDDSNXTISGTRR
TTOTOCHMANGVGTVSTLCKIRTYSTERGRAFGRUTTRGKLPDFMDCPAALYQL
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MLDCWGKDRNNRPKFEQITAGYSTERFYWEMSNQDVIKAVDEGYRLPPMDCPAALYQL
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Location/Qualifiers
                                                                                                                  9 from patent US
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/db_xref="GI:1247487"
/db_xref="SWISS-PROT:P29320"
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/codon_start=1
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/db_xref="taxon:9606"
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1 (Dases 1 to 3149)
Wicks, I.P., Wilkinson, D., Salvaris, E. and Boyd, A.W.
Molecular cloning of HEK, the gene encoding a receptor tyrosine
kinase expressed by human lymphoid tumor cell lines
proc. Natl. Acad. Sci. U.S.A. 89 (5), 1611-1615 (1992)
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Human receptor tyrosine kinase (НЕК) mRNA, complete cds
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Homo sapiens lymphoid tumor cDNA to
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Similarity 100.0%; Pred. No. 2.3e-15;
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//PICHUTE-TICEPTOR PICTIANDESTIQGELGW
//TANSALATION-TICEPTOR PICTIANDESTIQMELGEN
ISYPSHGWEEISGVDEHYTPIRTYQVCNVMDHSQNUWLETUWVPRNSAQKIYVELKFT
LENDCNSIFUYLGCEKETNLYYMESDDDHGVKFERHQFETNIDTIANDESGTQMDLGDR
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TTTCDUNGNORNNRPKFEGIVSILDKIRRPGSLKIITSAARAPSNLLLDGSNVDISTER
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101. .3052
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/db_xref="taxon:9606"
/cell_line="LK63"
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Sajjadi, F.G., Pasquale, E.B. and Subramani, S. Identification of a new eph-related receptor tyrosine kinase encodes and chicken that is developmentally regulated and New Biol. 3, 769-778 (1991)
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56; Conservative
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INETSYILDWSWPLDTGGRKDVFFNIICKKCGGSSKICEPCSDNYRELPROTGLTNYT
VTVUDLLAHTNYTFEIDAVNGVSDLSTLSRQFAAVSITTNQAAPSPITVIKDRTSRN
SVSLSWQEPEHPNGIILDYEVKYYEKQEDETSYTILRAKSTNYTIGGLKDDTTYPFQI
RARTAARYGTSSRKFEFETSPDSFSISSENSQVYMIAISAAVAIILLTVVVYVLIGRF
CGYKKSKHGTDEKRLHFGNGHLKLPGLRTYVDPHTYEDPNQAVHEFAKELDASNISID
KVVGAGEFGEVCSGRIKLPSKKEISVAIKTLKAGYTEKQREDFLAGASHLKLDGNHNI
IRLEGVYTKSKPVMIVTEYMENGSLDSFLRKHDAQFTVIQLVGMLRGIASGMKYLSDM
GYVHRDLAARNILINSNIVCKVSDFGLSRVLEDDPEAAYTTRGGRIP IRWTSPEALAY
RKFTSASDAWSYGIULWEVMSYGERPYMEMSFODVIKAVDEGYRLPPMDCPAALYQL
MLDCWQKDRNNRPKFEQIVSILDKLIRNPSSLKIITNAAARPSNLLDQSSINDISAFR
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/protein_id="AAA4866.1"
/protein_id="AAA4866.1"
/db_xref="Gi:211447"
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/translation="MDRRRLPLYMBSDDDHLAKFREHOFTKIDTIAADESTYUMLSAFPDTYDMD
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/translation="MDRRRLPLY"
/translation="M
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/db_xref="taxon:9031"
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On Feb 16
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Sequence
I15007
                                  Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2032)
Sajjadi,F.G., Pasquale,E.B. and Subramani,S. Identification of a new eph-related receptor tyrosine kinase from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor New Biol. 3, 769-778 (1991)
                                                                                                                                                                                                    complete cds.
M68515
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Mouse eph-related receptor
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Pasquale, E.B. and Sajjadi, F.G.
Eph-related tyrosine kinases, nucleotide sequences and methods
                                                                                                                                       Mus musculus
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Mus musculus (strain IRC
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M68513.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59;
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 3197)
Sajjadi, F.G., Pasquale, E.B. and Subramani, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor tyrosine kinase.
Mus musculus (strain IRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUSMEK4 3197
Mouse eph-related
                                                                                                                                                                                                                                                                                               Identification of a new eph-related receptor tyrosine kinase from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor New Biol. 3, 769-778 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                   /organism="Mus musculus"
/strain="IRC x Swiss Webster"
/db_xref="taxon:10090"
/dev_stage="11.5 day embryo"
/tissue_type="embryo"
89. .3040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_
                                                                                              /gene="Mek4"
89. .3040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INETSVILDMSWPLDTGGRKDITFNIICKKCGWNVRQCEPCSPNVRFLPRQLGLTNTT
VTVTDLLAHTNYTFEIDAVNGVSELSSPPRQYAAVSITINQAAPSPVMTIKKDRTSRN
SISLSWQEPEHPNGIILDYEVKYYQKQEQETSYTILRARGTNVTISSLKPDTTYVFQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMD
SQSLVEVRGSCVNNSKEEDPPRMYCSTEGEWLVPIGKCTCNAGYEERGFICQACRPGF
YKASDGAAKCAKCPPHSSTQEDGSMNCRCENNYFRAEKDPPSMACARPPSAPRNVISN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="Mek4 secreted"
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IRDCNSIPLVILGTCKETFNLLYYMESDDHGVKFREHQFTKIDTIAADESFTQMDLGDRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RARTAAGYGTNSRKFEFETSPDCMYYFSF"
2010. .2015
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/tlssue_type="embryo"
/codon_start=1
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/db_xref="GI:199120"
                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GI:199119
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lated receptor tyrosine kinase
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Pred. No. 5.3e-11;
0; Mismatches 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Mek4) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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JOURNAL
MEDLINE
REFERENCE
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AUTHORS
TITLE
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ORGANISM
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RNU69278
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ORIGIN
                                                                                                                                                                                                                                                                                 FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
TITLE
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Best Local
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                                                                                        SgS
                                                                                                                               gene
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Rattus norveg
(Rek4) mRNA,
U69278
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 3077)
L1,Y.Y., McTiernan,C.F. and Feldman,A.M.
IL-1 beta alters the expression of the receptor gene r-EphA3 in neonatal rat cardiomyocytes Am. J. Physiol. 274 (1), H331-H341 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 Similarity
59; Conser
                                                                                                                                                                                                                                                                                            Submitted (01-SEP-1996) Cardiology, University of Pittsburgh, Lothrop Street, Pittsburgh, PA 15213, USA On Apr 18, 1997 this sequence version replaced gi:1698721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                Li,Y.Y., McTiernan,C.F.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U69278.1 GI:1943913
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INETSVILLMSRPLDTGGRKDITFNIICKKCGMNVRQCEPCSPWNRFLPRQLGLTNTT
TYTTDLLAHTNUTTFELDAVNGVSELSSPRQVAAVSITINQAAPSPWRTLFRACGTITKORTSR
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RARTAAGYGTNSRKFEFETSDSFSIGGENSHVMIAISAAVAITIVLTVTYVLVGRF
CGYHKSHKSAEEKRLHFGNGHLKLPGLRTYVDPHTYEDFDAVHEFAKELDATNISID
KVVGAGEFGEVCSGRLKLPSKKEISVAIKTLKVGYTEKQRRDFLGEASIMGQFDHPNI
TRLEGVTKSKPEMIVTEYMENGSLDSFLRKHDAQFTVIQLVGKIFGLASGMKYLSDM
GYVHRDLAARNILINSNLVCKVSDFGLSRVLEDDPEAAYTTGGKLFIRMTSPEAMSY
KKTTSASDVWSYGIULMEVYMSYGERFYSQMSNQDVIKAVDEKYRLPPMDCPAALYQL
HLDGWONDRNNRPKFEDIVSILDKLIRNFGSIKIITSAAARFNLLLDQSNVDIATFH
MLDGWONDRNNRPKFEDIVSILDKLIRNFGSIKITTSAAARFNLLLDGSNVDIATFH
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LKLNTEIREVGPVNKKGFYLAFQDVGACVALVSVRVYFKKCPETVKNLAMFPDTVPMD
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35. .2989
                                                                                                                                                                       /strain-"Sprague-Dawley"
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/gene-"Rek4"
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/product-"eph-related receptor tyrosine kinase homolog"
/protein_id-"AAC06273.1"
                                                                                                                                                   /cell
                                                                                                                                                                                                                                                                            Location/Qualifiers
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ISYPSHGWEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFT
                                                                                                                                                                                                                                     /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                             .3077
                                                                                     . 2989
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                                                                                                                                                   _type="cardiomyocytes"
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Pred. No. 5.5e
0; Mismatches
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5.5e-11;
hes 7;
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Rattus.
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 CACGGG 187
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136644.1 GI:551611
EPH-11ke receptor PTK; receptor protein-tyrosine kinase.
Homo sapiens (clone library: Stratagene premade library, cat
#936206) female fetus, 17-18 weeks gestation brain cDNA to m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor protein-tyrosine kinases
Oncogene 10 (5), 897-905 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA cloning and tissue distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3162)

FOX,G.M., Holst,P.L., Chute,H.T., Lindberg,R.A., Janssen,A.M.
Basu,R. and Welcher,A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo
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sapiens receptor protein-tyrosine kinase (HEK7) mRNA, 3'
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ILKLNTEIREFGPVNKKGFYLAFQDVGACVALVSVVYEKKCPFTYKNLAMEPDTVPM
IKKLNTEIREFGPVNKKGFYLAFQDVGACVALVSVVYEKKCPFTYKNLAMEPDTVPM
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TYTYTDLLAHTNYTFEIDAINGVSELSSPPRQFAAVSITTNQAAPSPVMTIKKDRTSR
NSISLSWQEPEHPNGIILDYEVXXYEKOBQETSYTILRARGTNVTISSLKRDTTYVFQ
IRARTAAGYGTNSKKEEFENSPDSFSISGENSHYWAIAISAAVAIIVLTVTYTYLLYGR
FCGYHKSKHSSDEKRLHFGNGHLRLPGLTYVDPHYEDDFQAVHEFAKELDATNIAI
DKVVGAGEFGEVCSGRLKLPSKKEISVALKTLKVGYTEKORRDFLGEASINGQFDHEN
IRLEGVTKSKHSDEKRLHPSMENGSLDSFLRKHDAGFTVJOLVGMLRGTASGMKYLSD
MGYVHRDLAARNILINSNLVCKVSDFGLSRVLEDDFAAYTTRGGKIPVRMTSPEATA
YRKFTSASDVWSGIVALWEWMSTGERFYWEMSNODVIKAVDEGXBLDLPHDCDFAALYQ
LMLDCWGKDRNNRFKERGIVSILDKLLRNGSLKIITSAARRESHLLDQSNVDLATF
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714 c
/codon_start=1
/product="receptor protein-tyrosine kinase"
/protein_id="AAA74245.1"
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/db_xref="taxon:9606"
/dev_stage-"fetus, 17-18 weeks gestation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTTGDWLNGMRTAHCKEIFTGVEYSSCDTIAKISTDDMKKVGVTVVGPQKKIISSIKA
                                                                                                                       /gene="HEK7"
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/tissue_type="brain"
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                                                                                                                                                                    product="receptor protein-tyrosine kinase"
                                                                                                                                                                                                /gene="HEK7"
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Pred. No. 2.3e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of five human EPH-like
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RESULT HUMRPTKB

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Matches

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Partial human EHK-1 cDNA without information on mRNA splicing variants has been published by Fox, G.M. et al. (1995). Oncogene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46;
                                                                                                                                                                                                                                                                                                             Miescher Constant, G. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                               Extensive splice variation and localization of the EHK-1 receptor tyrosine kinase in adult human brain and glial tumors Brain Res. Mol. Brain Res. 46 (1-2), 17-24 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H.sapiens mRNA for El
X95425
X95425.1 GI:1177465
                                                                                                                                                        variants has been published by 10:897-905.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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RQSGLKNTSVMMVDLLAHTNITE I EAVROLEGARQYVEVTTNQAABSSVTIN
VKKKIAKNSISLSWGEDDRPNGIILEYEIKHEFENDETSYTIIKSKETITABGLKV
VKKKIAKNSISLSWGEDDRPNGIILEYEIKHEFENDETSYTIIKSKETITABGLKV
ASVYVFQIFARTAAGYGVFSRRFEFETTPVFAASSDQSQIPVIAVSVTVGVIILLAVVI
GVLLSGREGGYESKAKDDPEEEMHFHRGIIKLPGVRTIIDPHTYETKORNDPAGAVHEFAKEI
EASCITIERVIGAGEFEGEVCSGRLKLPGKRELFVAIKTIKVGYTEKORNDFLGEASIN
EAGCITIERVIGAGEFEGEVCSGRLKLPGKRELFVAIKTIKKNDGQFTVIQLVGMLRGISA
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TAPEAIAFRKFTSASDVWSYGIVMWEVVSYGERPYWEMTNQDVIKAVEEGYRLPSPMD
CPAALYQLMLDCWQKERNSRPKFDEIVNMLDKLIRNPSSLKTLVNASCRVSNLLAEHS
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="4"
/clone_lib="lambda ZAPII #936206"
/clone="HFB415"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="HEK7"
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Na for EHK-1 receptor
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Best Local Similarity
Matches 46; Conserv
    AUTHORS
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CDS
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                                                                                                                          U03910.1
Eph.
                                                                                                                                                                                 GGCEK7B 4124 bp mRNP Gallus gallus receptor-type (Cek7) mRNP, complete cds.
Gallus gallus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus. 1 (bases 1 to 4124) Siever, D.A. and Verderame, M.F.
                                                                                                       chicken.
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2114. .2392
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1778 .2113
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GVVTKSKPVMIVTEYMENGSLDTFLKKNDGQFTVIQLVGMLRGISAGMKYLSDMGYVH
RDLAARNILINSNLVCKVSDFGLSRVLEDDPEAAYTTRGGKIPIRWTAPEAIAFRKFT
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KDQETSYTIIKSKETTITAEGLKPASVVFQIIARTAAGYGVESRFEEETTPVFAAS
SDQSQIPVIAVSVTVGVILLAVVIGVLLSGSCCECGCGRASSLCAVAHFILIWRCGYS
KAKQDPEEEKMHFHNGHIKLPGVRTYIDPHTYEDPNQAVHEFAKEIEASCITIERVIG
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SCVCEKDYFRRESDPTMACTRPPSAPRNAISNVNETSVFLEWIPPADTGGRKDVSYY
IACKKONSHAGVCEECGGHVRYLPRQSGLKNTSVMVDLLAHTNYTFEIEAVNGVSDL
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KVMEQNQNUMLLTSWISNEGASRIFIELKFTILRDCNSLPGGLGTCKETRMYYFESDD
QNGRNIKENQYIKIDTIAADESFTELDLGDRVMKLNTEVRDVGPLSKKGFYLAFQDVG
ACIALVSVRVYYKKCPSVVRHLAVFPDTITGADSSQLLEVSGSCVNHSVTDEPPKMHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="RNA splice domain IIb"
2502. .2567
/note="RNA splice domain III"
882 c 953 g 977 t
                                                                                                                                               GI:555617
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WQKERNSRPKFDEIVNMLDKLIRNPSSLKTLVNASCRVSNLLAEHSPLGSGAYRSVGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="EHK-1 receptor tyrosine kinase"
/protein_id="CAA64700.1"
/db_xref="GI:1177466"
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/clone="HFB129"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="SWISS-PROT:P54756"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="brain"
/cell_type="CNS neurons"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MRGSGPRGAGHRRPPSGGGDTPITPASLAGCYSAPRRAPLWTCL"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identification of a complete Cek7 receptor protein tyrosine kinase coding sequence and cDNAs of alternatively spliced transcripts Gene 148 (2), 219-226 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Siever, D.A.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="receptor-type protein-tyrosine kinase"
/product="receptor-type protein-tyrosine kinase"
/protein_id="RAB60614.1"
/db_xref="g1:55620"
/db_xref="g1:55620"
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/VMGDLGWIAYPKNGWEEIGEVDENYAPIHTYOVCKVMEDONNWLLTSWISNEGRRAS
SFELKFTLRDCNSLPGGLGTCKETFNMYFESDDEDGRNIRENQYIKIDTIAADESFT
ELDLGDRVMKLMTEVROVGPLTKKGFYLAFQDVGACIALVSVRVYYKCPSVIRNLAR
FPDTITGADSSOLLEVSGVCVNHSVTDEAPKMHCSAEGEWLVPIGKCLCKAGYEEKNN
TCQAPSTVSSVKKGKITNASISLSWQEEDRPWIZILIEVFTFENDQGSOLFIIVSVT
TAITADGLKPGSAYVFOIRARTAAGYGGESTRREEFETSPVLAASSOGSOLFIIVSVT
VGVILLAVVIGFLLSGRRCGYSKAKQDFEEKMHFHNGHIKLPGVRTYIDPHTYEDPN
QAVHEEAKEIEASCITLERVIGAGEFGEVGSGLKLOGKREEFVAIKTLKVGYTEXOR
RDFLGEASIMGGPHPNIIHLEGVYTKSKEVMHTVETXMENGSLDTFLKKNDGOFTVIQ
LVGMLRGIASGKYLSDMGYVHADLAARNILINSNLVCKVSDFGLSRVLEDDPEAAYT
TRGGKLFIRWTAPEALAFRKFTSASDVWSYGIVMEVMSYGERFYWEMTNODVIKAVE
TRGGKLFIRWTAPEALAFRKFTSASDVWSYGIVMEVMSYGERFYWEMTNODVIKAVE
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/tissue_type="body wall"
/dev_stage="ten-day embryo"
/note="this sequence diverges 3' of nucleotide 3023 when compared with previously reported Cek7 sequence (GenBank Accession Number Z19058)"
SAPRSAISNIVNETSVELEMIPPADTGGRKDVSYYIACKKCNSHSGLCEACGSHVRYLP
QQTGLKNTSVMAVDLLAHTNITEILAVNGVSQNYGGARQFVSNVTTRQAAPSSVSS
VKKGKITKNSLSLSWQEPDRENGIILEYEIKYEEKDGETSYTIIKSKETAITADGLKK
GKRYTGHARTAAGYGGFSRRFEEFETSPVLAASSDQSQIPIIVVSVTVGVILLAVVI
GFLLSGSCCDHGCGWASSLRAVAYEDTIMRCGYSKAKQDPEEEKMHFHNGHIKLDEVRI
TYIDHTYEDDNQAVHEFAKBIEASCITIEKVIGAGEFEGEVCSGRLKLOGKREEPPAI
KTLKVGYTEKQRRDFLGEASIMGQFDHPNIIHLEGVVTKSKPVMIVTEYMENGSLDTF
                                                                                                                                                                                                                                            ELDLGDRVMKLNTEVRDVGPLTKKGFYLAFQDVGACIALVSVRVYYKKCPSVIRNLAR
FPDTITGADSSQLLEVSGVCVNHSVTDEAPKMHCSAEGEWLVPIGKCLCKAGYEEKNN
TCQVCRPGFFKASPHSPSCSKCPPHSYTLDEASTSCLCEEHYFRRESDPPTMACTRPP
                                                                                                                                                                                                                                                                                                                                                /translation="mglrggggraggpapgwtclllcaalrsllaspgsevnlldsrt
Vmgdlgwiaypkngweeigevdenyapihtyqvckvmeqnqnnwlltswisnegrpas
Sfelkftlrdcnslpgglgtcketfnwyyfesddedgrnirengyikidtiaadesft
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85. .3126
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RVSNLLVEHSPVGSGAYRSVGEWLEAIKMGRYTEIFMENGYSSMDSVAQVTLEDLRRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="receptor-type protein-tyrosine kinase"
/protein_id="AAB60612.1"
/db_xref="GI:555618"
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(insertion A) and nucleotides 1802-1867 (insertion B)"
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/db_xref="taxon:9031"
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/codon_start=1
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VMGDLGWIARPKNGWEEIGEVDENYAPIHTYQVCKVMENQNNWILTSWISNEGRRAS
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TCQVCKPGFFKASPHSPSCSKCPPHSYTLDEASTSCLCEEHYFRRESDPTMACTRP
SAPRSAISNVMETSVFLEWIPPADTGGRKDVSYIACKKCNSHSGLCEACGSHVRYLP
QQTGLKNTSVMMVDLLAHTNYTEFIEAVKGVSDQNFGARQFVSVNVTTNQAAPSPVSS
VKKGKITKNSISLSWQEEDRPNKGIILEYEIKYFEKDQETSYTIKGKETAITADGLKP
GSAYVFQIRARTAAGYGGFSRRFEFETSFVLAASKOQPEDYTIKGKETAITADGLKP
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EASCITIERVIGAGEFGEVCSGRLKLQGKREFPVAIKTLKVGYTEKQRDFLGEASIM
GQFDHHNIIHLEGVYTKSKFVMINGTYTENBINGSLDTFLKKNDGQFTVIQLVGMLRGIAS
GMKYLSDMGYVHRDLAARNILINSMLVCKVSDFGLSKVLEDDFEAAYTTRGGKIPIKM
TAPEALAFKFTSASDVWSYGITWMEVMSYGERFWEMTWQDVIKANSEGYRLLFSPMD
CDAALYQLMLDCWGKDBNSRPKDEIVSMLDKLLRNSKLTLVANSUSKTLUSHS
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CDAALYQLMLDCWGKDBNSRPKDEIVSMLDKLLRNSKLTUNDASSTYSLLLSHS
CDAALYQLMLDCWGKDBNSRPKDEIVSMLDKLLRNSKLTUNDASSTYSLLLYSHS
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/note="polymorphism i
does not alter the an
/replace="t"
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/note="hydrophobic region characteristic of
transmembrane domain"
3127. .4124
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/product="protein-tyrosine kinase precursor"
85. .177
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does not alter the a
/replace="t"
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EMTNQDVIKAVEEGYKLPSPMDCPAALYQLMLDCWQKDKNERKFDEIVSMLDKLIRN
PSSLKTLVNASSRVSNLLVEHSPVGSGAYRSYGEWLBAIKMGRYTEIFMENGYSSMDS
VAQVTLEDLRRLGVTLVGHQKKIMNSLQEMKVQLVNGMVPL"
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                                                                                                                                                                                                                                                                                                                                                                           /note="polymorphism in third position of
does not alter the amino acid sequence"
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join(85. .1801,1868. .3126)
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1726. .1797
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Submitted (23-SEP-1996) Molecular Oncology,
P.O. Box 4000, Princeton, NJ 08543, USA
Location/Qualifiers
                                                                                                                                                                45; Conserv
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Eukaryota; Metazoa;
Eutheria; Rodentia;
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GADSSSLVEVRGQCVRHSEERDĪPKMYCSAGGEMUPDIGKCVCSAGYEERDJACMACE
LGFYKSARGDQLCARCPPHSHAGT FDAOTCRCDLSYVRALDPPSAACTRFPSAAPNL
ISSVNGTSVILLEWAPPLDPGGRSDITYNAVCRRCPWALSHCEACGSGTRFVPQQTSLA
QASLLVANLLAHMYSEWIEAVVGVSNLSPEPRSAVVNITTŅOAPSQVVVLRQERA
GQTSVSLLWQBEEQPHGILIEXFEIKYYEKDKEMOSYSTLKAVTTRATVSGLKPGTRYV
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FTREIEASRIHIEKIIGSGESGEVCYGRLQVFORDVFVLKALKAGYTERQRODFLS
EAAIMGQTDHPNITRLEGVVTRGRLAMIVTEYMENGSLDAFLRTHDGQFTIVQLVGML
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TLRDCNSIPGVLGTCKETFNLHYLESDRDLGASTQESQFLKIDTIAADESFTGADLGV
                                                                                                                                                                                                                                                                                     GITLMGHQKKILGSIQTMRAQLSSTQGRRRHL"
1504 c 1381 g 881 t
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PAPWGCPRALHQLMLDCWHKDRAQRPRFAHVVSVLDALVHSPESLRATATVSRCPPPA
FARSCFDLRAGGSGNGDLTVGDWLDSIRMGRYRDHFAAGGYSSLGMVLRMNAQDVRAL
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79. .3093
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Eph-and
                                                                                                                                                                                 49.1%;
68.2%;
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Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Elk-related kinase (eek) mRNA, complete cds.
                                                                                                                                                            Score 32.4; DB 12;
Pred. No. 0.033;
0; Mismatches 21;
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                                                                                                                                                                                              Length
                                                                                                                                                              Indels
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                                                                                                                                                                                                    4737;
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HS61A9/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (22-Nov-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enguiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 15, 1999 this sequence version replaced gi:6114770.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the feature by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Mp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chrl
RP1-61A9 is from the library RPC1-1 constructed at the Roswell Park Cancer Institute by the group of Pleter de Jong. For further details see http://bacpac.med.buffalo.edu/
VECTOR: pCYPAC2
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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/note-"Tandem repeat. Forced join. G: Restriction digest to be 1200-1500bp complement(82130. 82878) /note-"match: GSS: Em:AQ750854.1" complement(82496. 82871)
                                                                                                                                         complement(51292)
                                                                                                                                                          /note="match: GSS: Em:AQ816982.1"
                                                                                                                                                                                                                                                                                                         /note="match: GSS: 29241. .29448
                                                                                                                                                                                                                                                                                                                                                            /note="match: GSS: Em:AQ010082"
25683. .25889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(939.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
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/clone="RP1-61A9"
                                                                                                                                                                                                                   'note="Single clone region"
                                                                                                                                                                                                                                                                                                                                                                                                                                            note="match: GSS: Em:AQ134928"
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                                                                                                         Gap sized
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                                                         EPH-like receptor PTK; receptor protein-tyrosine kinase. Homo sapiens female fetus, 17\text{-}18 weeks gestation brain c
                                                                                                                                    Homo sapiens receptor
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                Homo sapiens
                                                                                                          L36642
                                                                                                                      complete cds.
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82591. .82878
/note="match: 0
86392. .86712
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complement(152202.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="match: GSS: Em:AQ746639.1

complement(13835. 138703)

/note="match: GSS: Em:AQ214151"

complement(138397. 138766)
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complement(121941.
                                                                                         GI:551607
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130376. .130747
/note=""""
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/note="match: G:
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147098. .147635
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138773. .1392
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130586. .131194
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/note="match: G
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                                                                                                                                                                                                                                                                                                                                           Score 32.4; DB 10;
Pred. No. 0.044;
0; Mismatches 21;
                                                                                                                                    protein-tyrosine kinase (HEK11) mRNA,
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RESULT 15
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nes 42; Conserv
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                                                                                                                                                  HSJ189K14 116490 bp DNA HTG
Homo sapiens chromosome 6 clone RP1-189K14,
PROGRESS ***, 6 unordered pieces.
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Fox, G.M., Holst, P.L., Ch
Basu, R. and Welcher, A.A.
                                                                                                            AL121966.1 GI:6981849
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                             Homo sapiens
                                                                   human.
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                                                                                        HTGS_PHASE1.
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TGLEDNYUTVMDLLAHANYTEEVEAVNGVSDLSRSGYELFAAVSITTGQAAPSOVSOVM
KERVLORSVELSWQEFEHPNGVITEYEIKYYEKDORERTYSTVKTKSTSASINNLKSG
TYYVEQIRAFTAAGYGNYSPRLDVATLEEATGKMFEATAVSSEQNPVIIIAVVAVAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GERKMKLNTEVREIGPLSKKGFYLAFQDVGACIALVSVKVYYKKCWSIIENLAIFPDT
VTGSEFSSLVEVRGTCVSSAEEEAENAPRMHCSAEGEWLVPIGKCICKAGYQQKGDTC
EPCGRGFYKSSSQDLQCSRCFTHSFSDKEGSSRCECEDGYYRAPSDPPYVACTRPPSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVRWTAPEAIQYRKFTSASDVWSYGIVMWEVMSYGERPYWDMSNQDVIKAIEEGYRLP
APMDCPAGLHQLMLDCWQKERAERPKFEQIVGILDKMIRNPNSLKTPLGTCSRPISPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IILVFMVFGFIIGRRHCGYSKADQEGDEELYFHFKFPGTKTYIDPETYEDPNRAVHQFAKELDASCIKIERVIGAGEFGEVCSGRLKLPGKRDVAVAIKTLKVGYTEKQRRDFLCEASIMGQFDHPNVVHLEGVVTRGKPVMIVIEFMENGALDAFLRKHDGQFTYIQLVGMLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MYFQTRYPSWIILCYIWILRFAHTGEAQAAKEVLLLDSKAQQTE
LEWISSPPNGWEEISGLDENYTPIRTYQVCQVMEPNQNNWLRTNWISKGNAQRIFVEL
KFTLKDCNSLPGVLGTCKETFNLYYEIDYDTGRNIRENLYVKIDTIAADESFTQGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HQKKIMSSIQTMRAQMLHLHGTGIQV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/product="receptor protein-tyrosine kinase"
/protein_id="AAA74243.1"
/db_xref="GI:551608"
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186. .3182
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/tlssue_type="brain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="receptor"
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Pred. No. 0.097;
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                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
Search completed: May 15, Job time: 18621 sec
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JOURNAL
                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                        Matches
                                                                                                                         15905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                             AL Submitted (16-OCT-1999) Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquires:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Feb 16, 2000 this sequence version replaced gi:006105.
IMPORTANT: This sequence is unfinished and does not necessarily
represent the correct sequence. Work on the sequence is in progress
and the release of this data is based on the understanding that the
sequence may change as work continues. The sequence may be
contaminated with foreign sequence from E.coli, yeast, vector,
phage etc. Order of seqments is not known; 800 n's separate
segments. Unfinished: dJ189K14 Contig_ID: 00235
Length: 4081 bp Unfinished: dJ189K14 Contig_ID: 00235
acc=AL121966 Length: 19639 bp Unfinished: dJ189K14 Contig_ID: 00370
acc=AL121966 Length: 26994 bp Unfinished: dJ189K14
Contig_ID: 00919 acc=AL121966 Length: 31021 bp Unfinished:
dJ189K14 Contig_ID: 01165 acc=AL121966 Length: 29139 bp
Unfinished: dJ189K14 Contig_ID: 01338 acc=AL121966 Length: 1616
                                                                                                                      CTGCTGGATTCTAAAGCACAACAACAGAGTTGGAGTGGATTTCCTCTCCACCCAATGGG 15964
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sims, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                be preserved
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114875 116400
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25321 52314: contig of 26994 bp in length
52315 53114: gap of 800 bp
53115 84135: contig of 31021 bp in length
84136 84935: gap of 800 bp
84136 84935: gap of 800 bp
114074: contig of 29135 bp in length
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4082 4881: gap of 800 bp
4882 24520: contig of 19639 bp in length
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18571 c 20111 g
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Location/Qualifiers
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                                                                                                                                                                                                                                          47.3%;
70.0%;
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Maximum
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Copyright (c) 1993 - 2000
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46. 9b_estL77.
48. 9b_estL78.
48. 9b_estL88.
48. 9b_estL89.
49. 9b_estL99.
50. 9b_estL11.
51. 9b_estL22.
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55. em_estL3.
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66. em_estL3.
66. em_estL8.
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71. 9b_estL3.
72. 9b_estL3.
73. 9b_estL3.
74. 9b_estL4.
75. em_estL89.
76. em_estL99.
77. em_estL89.
7
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                   RESULT
AU080921
LOCUS
                                                                                                                                                                                                                                   ACCESSION
VERSION
                                     COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mai
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
E 1 (bases 1 to 835)
S Hashimoto, K., Kusuda, J., Toyoda, A., Tanuma, R., Ito, A.,
Suzuki, Y., Sasaki, M. and Sugano, S.
Isolation of full-length cDNA clones from a mouse brai
library made by oligo-capping method
Unpublished (1999)
Unpublished (1999)
Contact: Ratsuyuki Hashimoto
Division of Genetic Resources
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AIO11632 EST206083
AIO11632 EST206083
R15319 yf88e12.x1
AI325344 m101c02.x
AI325344 m101c02.x
AI325344 m101c02.x
AI323334 m101c02.x
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AI323334 m101c02.x
AI326337 ILO-HT015
AW045268 UI-M-BH1-H25851 yf53903.s1
AW233440 ff332f03.y
AID2640428 DEF2p434C
AIB28089 wX31f07.x
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AIB28089 wX31f07.x
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AICO2549 AI88A09.s
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/lab_host="TOP10"
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/clone="MNCb-6241"
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/strain="C57BL"
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Location/Qualifiers
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Pred. No. 6.5e
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National Institute of Infectious Diseases 23-1, Toyama 1-chome, Shinjuku-Ku, Tokyo 162-8640, Japan 23-1, Toyama 1-chome, Shinjuku-Ku, Tokyo 162-8640, Japan Email: khashlenih.go.jp
                                                                                                                                                     /note="Organ: brain; Vector: pME18S-FL3; 1st strand cDNA
was primed with an oligo(dT) primer
[ANGTGGCCTTTTTTTTTTTTTTTTTTT] double-stranded cDNA was
ligated to a DrailI adaptor [TGTTGGCCTACTGG] , digested
and cloned into dstinct DrailI sites of the pME18S-FL3.
xhoI sites just outside the DrailI sites can be used to
isolate the cDNA insert. Size selection was performed to
exclude fragments <1.5 kb. Library was constructed by
Sugano et al. (University of Tokyo, Institute of Medical
Science). Custom primer for sequencing: 5' end primer
[CTTCTGCTCTAAAACCTGCG]"

02 a 182 c 230 g 190 t 31 others
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/sex="female"
Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
Insert Size: 2663
High quality sequence stops: 276
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2663 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1995)
On May 5, 1995 this sequence version replaced gi:797807
Contact: Wilson RK
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1 (bases 1 to 435)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Farsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Travaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yp50g04.r1 Soares retina N2b4HR Homo sapiens cDNA clone IMAGE:190902 5' similar to gb:m83941 TYROSINE-PROTEIN KINASE RECEPTOR HEK PRECURSOR (HUMAN); , mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, Tel: 314 286 1800
Fax: 314 286 1810
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Location/Qualifiers
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                                                                                               University of Toronto. ____
Soares and M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="GDB:3847311"
/db_xref="taxon:9606"
/clone="IMAGE:190902"
                                                                                                                                                                                                                                                                                                                                                                                           /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Soares retina N2b4HR"
                   30.4%;
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Score 200.6; DB 23;
Pred. No. 1.3e-48;
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Hilier,L., Clifton,S., Allen,M., Gibbons,M., Joh
Martin,J., Pape,D., Steptoe,M., Underwood,K., Th
Ritter,E., Bowers,Y., Wylie,T., Waterston,R. and
WashU Zebrafish EST Project 1999
Unpublished (1999)
On Jun 5, 1998 this sequence version replaced gi
Other_ESTs: fi31907.x1
Contact: S.L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, M
Tel: 31, 286 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Library constructed by Dr. Sumio Suga
Sequencing by: Washington University
Seq primer: T3 ET from Amersham
High quality sequence stop: 485.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 314 286 1800
Fax: 314 286 1810
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1 (bases 1 to 572)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW175051 572 bp mRNA EST 16-NOV-1999 f131902.yl Sugano Kawakami zebrafish DRA Danio rerio cDNA clone 2639202 5' similar to SW:EDA4_CHICK Q07496 EPHRIN TYPE-A RECEPTOR 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Danio rerio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             zebrafish
/note-"Vector: pME18S FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dr) primer (ATGTGGCCTTTTTTTTTTTTTT];
                                                                                                                                                                                                                                                                     /clone_lib="Sugano Kawakami zebrafish DRA"
/sex="mixed (one male and one female, incluunfertilized eggs)"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                              /strain="AB"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                  /lab_host="DH10B (phage resistant)"
                                                                                                                                                                                                                                                                                                                                                        /clone="2639282"
                                                                                                                                                                                                                                                                                                                                                                                                                    ∕organism="Danio rerio"
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Iniversity Genome Sequencing Center
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              St. Louis, MO 63108, USA
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JOURNAL COMMENT
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Matches 257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGGGAAGAGGTGAGCATCATGGATGAGAAGAATACGCCAATCAGGGACGTCCCANGTGTG 255
                                                                                                                       Tagged Connectors
Unpublished (1997)
Contact: Mahairas GG, Zackrone KD,
University of Washington
Seartle, WA 98195, USA
Tel: (206) 616-8744
Fax: (206) 685-7301
Email: kzackron@u_washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTCACGCAGGTGGACATAGGAGACCGCATCATGAAGCTGAACACNGAGGTGAGGGATGT
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                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 424)

Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S., Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood, L.E. Construction of a Characterized Clone Resource for Genomic Sequencing; Generation and Preliminary Analysis of 20,000 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                          B36983 424 bp
HS-1042-A2-F05-MR.abi
sapiens genomic clone
                                                                                 Sequence Tagged Connector Plate: CT 824 row: K co. Class: BAC ends
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                                                     quality sequence stop: 424.
Location/Qualifiers
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a 136 c 160 g 104 t
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=CT 824 Col
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Pred. No. 9.4e-44;
0; Mismatches 105;
                                                                                               column: 10
 Col=10
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Best Local Similarity
Matches 233; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AI011631 474 bp mRNA EST206082 Normalized rat ovary, ROVAX55 3' end, mRNA sequence.
                                                                                                                                                                     The Institute for Genomic Research 9712, Medical Center Drive, Rockville, Tel: (301)-838-3529 Fax: (301)-838-0208
                                                                                                                                                                                                                                                                 Unpublished (1998)
On Jan 19, 1998 this sequence
                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 474)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M.,
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                            Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AI011631.1
                                                                                                                                                                                                                                                  Contact: Lee,
                                                                                                                                                                                                                                                                                                                Rat Genome Project:
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                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus sp.
                                                                                                                                       il: nhlee@tigr.org
primer: M13-21.
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E-Coli DH10B"
a 77 c 101 g
         /organism="Rattus sp."
/db_xref="ATCC (inhost):2021827"
/db_xref="taxon:10118"
/db_xref="RovAX55"
/clone="RovAX55"
/clone_llb="Normalized rat ovary, Bento Soares"
/note="Organ: ovary; Vector: pT7T3Pac; Site_1: EcoRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="CIT Human Genomic Sperm Library
/sex="M"
                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GI:3225463
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67.7%;
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Pred. No. 8.9e-32;
0; Mismatches 103
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                                                                                                                                                                                                    Unpublished (1998)
On Jan 19, 1998 thi
Contact: Lee, NH
ATCC
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EST206083
ROVAX56 3'
                                                                                                                                                                                                                                                                                                                                   Rattus sp. Rattus sp.
                                                                                                                                                   The Institute for Genomic Research 9712, Medical Center Drive, Rockvil Tel: (301)-838-3529
Fax: (301)-838-0208
                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Verteutheria; Rodentia; Sciurognathi; Muridae; M. 1 (bases 1 to 473)
Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Kerlavage, A.R. and Adams, M.D.
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                                                                                                                               primer: M13-21.
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                                                                                                                                        nhlee@tigr.org
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      /note="Organ: ovary;
Site_2: NotI"
127 c 136 g
                                        /organism="Rattus sp."
/db_xref="ATCC (inhost):2021828"
/db_xref="taxon:10118"
/clone="ROVAX56"
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/clone=1ib="Normalized rat ovary
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R15219.1
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                                                                                                                                                                                                                                                  Email: est@watson.wustl.edu
Insert Size: 1695
High quality sequence stops: 337 Source: IMAGE Consortium,
This clone is available royalty-free through LLNL; contact
IMAGE Consortium (info@image.llnl.gov) for further informat
Insert Length: 1695
Std Error: 0.00
Seq primer: M13RP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Sep 21, 1992 this sequence version Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The WashU-Merck EST Project Unpublished (1995)
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1 (bases 1 to 402)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M.,

Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M.,

Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F.,

Parsons,J., Rifkin,E., Waterston,R., Williamson,A., Wohldmann,P. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School
4444 Forest Park Parkway, Box
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson, R.
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/clone_lib="Soares infant
/sex="female"
/dev_stage="73 days post n
                                                                          /db_xref="taxon:9606"
/clone="IMAGE:29543"
                                                                                                                         /organism="Homo sapiens"
/db_xref="GDB:401890"
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Pred. No. 9.2e-28;
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RESULT 8
AI325344/c
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                                                                                                                  On Jan 19, 1998 this sequence version repl
On Jan 19, 1998 this sequence version repl
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (Dases 1 to 406)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AI325344 406 bp mRNA EST 23-DEC-1998 mi01c02.yl Soares mouse placenta 4NbMpl3.5 14.5 Mus musculus clone IMAGE:459170 5' similar to gb:U07634 Mus musculus receptor-protein tyrosine kinase (MOUSE);, mRNA sequence. AI325344
                                                                                                                                                                                                                                                                        Theising, B., Wylle, T., Lennon, G., Waterston, R.
The Washu-HHMI Mouse EST Project
                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           house mouse.
Mus musculus
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Pred. No. 1.2e-24;
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Best Local Sim
Matches 171;
  TITLE
JOURNAL
                                                                                                                           AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tgtactacatggagtctgatgatgatcatggggtgaaatttcgagagcatcagtttacaa 271
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                                                                                                                                                                                                                                                                                  mANU/4123 366 bp mRNA EST 21-JAN-1997 m101c02.rl Soares mouse placenta 4NbMP13.5 14.5 Mus musculus clone IMAGE:459170 5' similar to gb:U07634 Mus musculus receptor-protein tyrosine kinase (MOUSE);, mRNA sequence. AA024123
                                                                                       Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 366)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Moore
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Seq primer: -40RP fr
                                                       Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B. Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                AA024123.1
EST.
Unpublished
                     The WashU-HHMI Mouse EST Project
                                          Waterston, R.
                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                       Mus musculus
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117 c 109 g 100 t 1 others
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/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco
1st strand cDNA was primed with a Not I - oligo(dT) pr
[5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:459170"
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/dev_stage="adult"
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(1996)
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Pred. No. 5.9e-23;
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                                                                                                                                                                                                                                                                                                                                                                                       tgagaacaaactgggtccccaggaactcagctcagaagatttatgtggagctcaagttca 151
                                                                                                                                                                                                                                                                                                                                                                    TCCGCACCAACTGGGTGTACCGGGAGGAGGCCGAGCGCATCTTTATTGAGCTCAAGTTCA 171
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                                                                                                                                                                                                                                                                                                            CGGTGCGAGACTGTAACAGCTTCCCGGGTGGCGCCAGCTCATGCAAAGAGACCTTCAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169;
                             (HUMAN);, mF
AI249967
AI249967.1
EST.
                                                                                 AI249967 493 bp mRNA EST 05-NOV-1998 qx47d02.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2004483 3' similar to gb:M59371 TYROSINE-PROTEIN KINASE RECEPTOR ECK PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On May 8, 1995 this sequence version replaced Contact: Marra M/Mouse EST project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Louis, Tel: 314 286 1800

Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxor:10090"
/clone="IMAGE:459170"
/clone_lib="Soares mouse p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T 3']; double-stranded cDNA was ligated to Eco RI a (Pharmacia), digested with Not I and cloned into th and Eco RI sites of the modified pT7T3 vector. Libr went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaido."

103 c 102 g 92 t
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with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
ist strand cDNA was primed with a Not I - oligo(dT) primer
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/dev_stage="adult"
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                                              GI:3846496
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                                                                     sequence
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Pred. No. 5.1e-22;
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SOURCE
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 348)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuo
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                            AI323334 348 bp mRNA EST 23-DEC-1990 mi01c02.x1 Soares mouse placenta 4NbMP13.5 14.5 Mus musculus clone IMAGE:459170 3' similar to 9b:M59371 TYROSINE-PROTEIN FRECEPTOR ECK PRECURSOR (HUMAN); 9b:U07634 Mus musculus
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
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1 (bases 1 to 493)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                              Mus musculus
                                                                                                                                                                                                                                                                              receptor-protein tyrosine kinase (MOUSE);, mRNA sequence
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Site_2: NotI; Cloned unidirectionally. Primer:
Average insert size 1.72 kb. Life Technologies
11548-013"
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/clone_lib="NCI_CGAP_Pan1"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Pred. No. 3.7e-18;
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                                                                                                                                                                                      CTCTACTATGCAGAGACAGATGTGGACTATGGCACCAACTTCCAGAAGCGCCAGTTCACC
AI337308 496 bp mRNA EST 18-MAR-1999 tb98b01.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:2062345 3' similar to SW:EPB2_HUMAN P29323 EPHRIN TYPE-B RECEPTOR 2 PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone was previously sequenced on data is from the 3' end Trace considered overall poor quality High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mouseest@watson.wustl.edu
This clone is available royalty free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
On Jan 17, 1998 this sequence version replaced gi:2043939.
Contact: Marra M./Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston, R.
The WashU-HHMI Mouse EST Project
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Fax: 314 286 1810
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94 c 93 g 74 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism-"Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:459170"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="placenta"
/dev_stage="adult"
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Pred. No. 5.8e-
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71 GTGGAGATGAAGTTTTCGGTGCGTGACTGCAGCAGCATCCCCAGCGTGCCTGGCTCCTGC 130
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                                    actcaaatggatcttggggaccgtattctgaagctcaacactgagattagagaagtaggt 363
                                                                                                                                                    gtgaaatttcgagagcatcagtttacaaagattgacaccattgcagctgatgaaagtttc 303
                                                                                                                                                                                                                                                                       aaggagacattcaacctgtactacatggagtctgatgatgatcatg------gg 243
                                                                                                                                                                                                                                                                                                                                                                                              gtggagctcaagttcactctacgagactgcaatagcattccattggttttaggaacttgc 195
TCCCAGGTGGACCTGGGTGGCCGCGTCATGAAAATCAACACCGAGGTGCGGAGCTTCGGA
                                                                                                                   CCCAACTGGATGGAGAATCCATGGGTGAAGGTGGATACCATTGCAGCCGACGAGGAGCTTC
                                                                                                                                                                                                                                   AAGGAGACCTTCAACCTCTATTACTATGAGGCTGACTTTGACTCGGCCACCAAGACCTTC 190
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Eukaryota; Metazoa;
Eutheria; Primates;
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National Cancer Institute, Cancer Genome Anat
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Tissue Procurement: Ilan Kirsch, M.D., Michael R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               www-bio.llnl.gov/bbrp/image/image.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: ECO RI; Plasmid DNA from the normalized library NOT_CGAP_CO10 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-105125, and 1144584-1143551). Subtraction by Bento Soares and M. Fatima Bonaldo. "a 141 c 148 g 103 t
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/lab_host="DH10B"
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/db_xref="taxon:9606"
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Pred. No. 8.3e-17;
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acagtgaagaatctggctatgtttccagacacggtacccatggactcccagtcc---
                                                    GACATAGGTGCCTGGCCATCCTCTCTCTCCGCATCTACTATAAGAAGTGCCCTGCC 358
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wullf04.x1 NCI_CGAP_GC6 F
similar to SW:EPA8_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Jun 5, 1998 this sequence version Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: -40UP from Gibco.
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-GCAP clone distribution
found through the I.M.A.G.E Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D.,
R. Emmert-Buck, M.D., Ph.D.
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Unpublished (199
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National Cancer Institute, Cancer Genome Anatomy
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                                                                                                                                                                                                                           /note-"Vector: pT/T3D-Pac (Pharmacia) with a modified /note-"Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="pooled germ
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="IMAGE: 2516671"
                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone_lib="NCI_CGAP_GC6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
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                                                                                                                                              Score 88.2; DB 63;
Pred. No. 1.6e-15;
                                                                                                                             Mismatches
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009127 EPHRIN TYPE-A RECEPTOR 8 PREC
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                                                                143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1999)
On Mar 16, 1998 this sequence version replaced Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Pr
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                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (http://www.ludwig.org.br/scripts/gethtml2.pl7t1=IL0&t2=IL0-HT0156-
251099-132-a12&t3=1999-10-25&t4=1)
Seq.primer: puc 18 forward
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
                                                              Conservative
                                                                                                                                                                                       73
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                                                                                                                                                                               /note-"Organ: head_neck; Vector: pucl8; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
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                                                                                  13.0%;
                                                          Score 86; DB
Pred. No. 6.6e
0; Mismatches
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                                                 DB 80; LC
, 6.6e-15;
, 95;
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ATGACATGCCGATCTACATGTACTCCGTGTGCAACGTGATGTCTGGCGACCAGGACAACT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mEST@mail.nih.gov
Oligo-dT track not found, Not I site shown in beginning of sequence
1s likely internal to the message. CDNA Library Preparation: M.B.
Soares Lab Clone distribution: NIH BMAP cDNA clones will be made
available by the means that is soon to be determined. When NIH
determines the means for distribution of the BMAP cDNA clones, this
record will be updated accordingly when that means is determined.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AW045268 314 bp. mRNA EST 18-SEP-1999 UI-M-BH1-akn-b-03-0-UI.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone UI-M-BH1-akn-b-03-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Jun 5, 1998 this sequence version
Contact: Chin, H
National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MS
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two appr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 301 443 1706 Fax: 301 443 9890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 6 (9), 791-806 (1996) 97044477
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Mus musculus
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                      72
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/note="vector: p773D-Pac (Pharmacia) with a modified
/note="vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Ecc RI; The
NIH_BMAP_M_S1 library is a subtracted library derived from
NIH_BMAP_M_S1 which in turn is a subtracted library
derived from a mixture of normalized libraries from ten
regions of the mouse brain (cerebellum, brain stems,
olfactory bulbs, hypothalamus, cortex, amygdala, basal
ganglia, pineal gland, striatum, hipoccampus). The driver
used for subtraction consisted of a pool of 5,000 clones
from the NIH_BMAP_M_S1 library and a pool of 2,000 clones
obtained from non-normalized and normalized mouse brain
spinal cord libraries.
TAG_LIB-NIH_BMAP_M_S2
TAG_TISSUE-olfactory-bulbs
                      Ø
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Best Local Similarity
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304 TCTACTA 310
                           212 tgtacta 218
                                                         244 CGGTGCGAGACTGTAACAGCTTCCCGGGTGGCGCCAGCTCATGCANAGAGACCTTCAACC 303
                                                                                                                  184 TCCGCACCAACTGGGTGTACCGGGAGGAGGCCGAGCGCATCTTATTGAGCTCAAGTTCA 243
                                                                                                                                                 92
                                                                                                                                                                                               32 acacacccatcaggacttaccaggtgtgcaatgtcatggaccacagtcaaaacaattggc 91
                                                                        tgagaacaaactgggtccccaggaactcagctcagaagatttatgtggagctcaagttca 151
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                                                                                                                                                                                                                                                   11.5%;
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Pred. No. 7.4e-12;
0; Mismatches 70;
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Search completed: May 15, 2000, 11:20:21 Job time: 19144 sec

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Result
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Sequence 34, Appl
Sequence 102, Appl
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Sequence 1, Appli
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Sequence 15, Appli
Sequence 16, Appli
Sequence 16, Appli
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US-08-167-919A-9
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79.8	79.8		79.8	98	117.6	117.6	117.6	117.6	117.6	117.6	119.8	138.4	138.4	168	168	168	186.8
12.1	12.1	12.1	12.1	14.8	17.8	17.8	17.8	17.8	17.8	17.8		•	21.0			25.5	• .
3969	3969	3969	3969	3133	4027	4027	4027	4027	2982	2982	3776	3591	3546	2962	2962	2962	4097
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PCT-US95-04228-23	US-08-436-054-5	US-08-222-616-23	US-08-436-044-5	US-08-162-809-1	US-08-571-785-4	US-08-571-785-3	US-08-348-143-4	US-08-348-143-3	•	US-08-348-143-2	US-08-162-809-7	US-08-162-809-13	US-08-162-809-9	PCT-US95-04681-10	US-08-702-367A-10	US-08-449-645A-10	US-08-162-809-11
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ALIGNMENTS

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Sequence 9, Application US/08167919A
PATENT NO. 5674691

GENERAL INFORMATION:
APPLICANT: Boyd, Andrew W.
APPLICANT: Wicks, Ian
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/167,919A
FILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PK8841 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION NUMBER: PK8841 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION NUMBER: PK8992 (AU)
PRIOR APPLICATION NUMBER: 9199
PRIOR APPLICATION NUMBER: 31,46
REFERENCE/DOCKET NUMBER: 9159
FELECOMMUNICATION INFORMATION:
NAME: DIG19110, Frank S.
REGISTRATION NUMBER: 31,46
REFERENCE/DOCKET NUMBER: 9159
FELECOMMUNICATION INFORMATION:
TELEBHOKE: (516) 742-4343
TELEBHOKE: (516) 742-4343
TELEBHOKE: (516) 742-4364
TELEBHOKE: (516) 742-4364
TELEBHOKE: (516) 742-4364
TELEBHOKE: G516) 742-4364
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400 Garden

City Plaza

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US-08-715-106-9

Sequence 9, Application US/08715106

Patent No. 6020306

; GENERAL INFRAMATION:
APPLICANT: Boyd, Andrew W.
APPLICANT: Simpson, Richard J.
APPLICANT: Wicks, Ian
APPLICANT: Ward, Larry D.
APPLICANT: Wilkinson, David
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; LOCATION:
US-08-167-919A-9
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Best Local Similarity 100.0%;
Matches 660; Conservative (
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      APPLICANT: Wicks, Ian
APPLICANT: Ward, Larry D.
APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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100..3048
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Scott,
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Pred. No. 8.7e-208;
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REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9159
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4346
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3132 base pairs
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Best Local S
Matches 660
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FILING DATE: 18-APR-1994
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-JUN-1991
FILING DATE: 21-JUN-1991
PRIOR APPLICATION NUMBER: PK9992 (AU)
FILING DATE: 12-DEC-1991
FILING DATE: 12-DEC-1991
PRIOR APPLICATION NUMBER: PCT/AU92/0029
APPLICATION NUMBER: PCT/AU92/0029
FILING DATE: 19-JUN-1992
ATTORNEY/ACENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: singl
TOPOLOGY: linear
MOLECULE TYPE: DNA (9)
FEATURE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0) CURRENT APPLICATION DATA:
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Local Similarity 100.0%; Pred. No. 8.7e-208;
les 660; Conservative 0; Mismatches 0;
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                                                                           9999tgaaatttcgagagcatcagtttacaaagattgacaccattgcagctgatgaaagt
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                                                           GGGGTGAAATTTCGAGAGCATCAGTTTACAAAGATTGACACCATTGCAGCTGATGAAAGT
                                                                                                                      GTTTTAGGAACTTGCAAGGAGACATTCAACCTGTACTACATGGAGTCTGATGATGATCAT
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100..3048
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                                                                                                                ; NAME/REY:
; LOCATION:
US-08-162-809-15
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US-08-162-809-15
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                                                         Query Match
Best Local
                                            Matches
                                                                                                                                                                                                TELEFAX: (619) 33 (15: INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS: SEQUENCE 3354 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 4370 La JOLla VILL
CITY: San Diego
STATE: California
COUNTRY: United States of
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Fereydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED
TITLE OF INVENTION: NUCLEOTIDE SEQUENC
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: P-LJ 9503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9901
TELEPAX: (619) 535-8949
                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           601
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                                           Local Similarity hes 537; Conserv
                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                            TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
tgggaagagatcagtggtggatgaacattacacacccatcaggacttaccaggtgtgc 60
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                                            Conservative
                                                                                                                            CDS
32..2980
                                                                                                                                                                      linear
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                                                        70.2%;
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                                           0;
                                          Score 463.2; DB 1;
Pred. No. 6.3e-143;
0; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drive,
                                                                                                                                                                                                                                                                                                                                                                                                           Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Suite
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                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application Patent No. 5981245 GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
EPILING DATE:
CLASSIFICATION: 435
ATTORRY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A
                                                                                                                    COMPUTER READABLE FORM:
MEDIOM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                        APPLICANT: FOX, GATY M.
TITLE OF INVENTION: EPH-Like
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
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ZIP: 91320
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CITY: Thousand Oaks
STATE: California
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1840 Dehavilland Drive
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                                                                                              US/08/449,645A
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RESULT 5
US-08-702-367A-14
; Sequence 14, Application US/08702367A
; Patent No. 5981246
; GENERAL INFORMATION: FOX, GATY M.
APPLICANT: FOX, GATY M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
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; TYPE: nucli:
; STRANDEDNESS
; TOPOLOGY: 1
; MOLECULE TYPE:
; FEATURE:
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LOCATION: 3
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Best Local Similarity

Matches 460; Conserv
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
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Pred. No. 4.7e-98;
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; LOCATION:
US-08-702-367A-14
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Best Local Similarity 69.4%;
Matches 460; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FC-DOS/MS-DOS
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ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STRIE: California
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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FILING DATE:
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Pred. No. 4.7e-98;
0; Mismatches 200;
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PCT-US95-04681-14
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                                                                                                                                                                                                                                                                             Query Match 49.5%;
Best Local Similarity 69.4%;
Matches 460; Conservative
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NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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CORRESPONDENCE ADDRESS:
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CLASSIFICATION:
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STATE: California
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                                                 9ttttäggaacttgcaaggagacattcaacctgtactacatggagtctgatgatgatcat 240
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Pred. No. 4.7e-98;
0; Mismatches 200;
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                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 kb fl
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION MATE: US/08/222,616
FILING DATE: 4-APR-1994
                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/00

FILING DATE: 22-JAN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/826935

FILING DATE: 22-JAN-1992

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.
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APPLICANT:
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TITLE OF INVENTION: ANTIBODIES
NUMBER OF SEQUENCES: 42
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                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                            CITY: South San Francisco
REFERENCE/DOCKET NUMBER:
                 REGISTRATION NUMBER:
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460 Point San Bruno Blvd
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Wood, William I
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TELEPHONE: 415/225-1994
TELEPAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 34
SEQUENCE CHARACTERISTICS:
LENGTH: 3348 bases
TYPE: nucleic acid
STRANDEDNESS: single
JOPOLOGY: linear
US-08-222-616-34
                             RESULT 8
PCT-US95-04228-34
; Sequence 34, Application
; GENERAL INFORMATION:
; GENERAL INFORMATION:
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Best Local S
Matches 460
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          Bennett, Brian D. Goeddel, David
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Pred. No. 4.9e-98;
0; Mismatches 200
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STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-04228-34
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FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 821P3P0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/25-1994
TELEFAX: 415/93-9881
TELEX: 910/371-7168
INFORMATION FEED NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 3348 bases
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Best Local Similarity
Matches 460; Conserv
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MEDIUM TYPE: 5.25 inch, 360 Kb fl
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/0422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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PRIOR APPLICATION DATA:
                                                                                                                                                                  340
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STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
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GGGCCATTAAGCAAAAAGGGGTTTTACCTGGCTTTTCAGGATGTGGGGGCCTGCATCGCC
              99tcctgtcaacaagaagggattttattttggcattttcaagatgttggtgcttgttgtctcc
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 Mismatches

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Pred. No. 4.9e-98;
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RESULT 9
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Patent No. 5843/**
GENERAL INFORMATION:
APPLICANT: Maisonpierre, et al
APPLICANT: MAISONPIERRAND RC
TOTAL OF INVENTION: KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 100, Application US/08469537A Patent No. 5843749
                                                                                                             INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 3592 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,537A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
FEATURE:
NAME/KEY:
                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: RETELECOMMUNICATION INFORMATION: 914-345-7400
                                                                                                                                                                                                                                          FILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Ph.D., Gall |
REGISTRATION NUMBER: 32,143
PREFERENCY DOCUMENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: USSN 0
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 0
FILING DATE: 28-CCT-1993
APPLICATION NUMBER: USSN 0
                                                         FEATURE:
                                                                      MOLECULE TYPE:
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                           NAME/KEY:
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OPERATING SYSTEM: DOS
                                                                                      TOPOLOGY:
                                                                                                  STRANDEDNESS:
                                                                                                                                                                                        TELEFAX: 914-345-7721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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777 Old Saw Mill River Road
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                                                                       unknown
E: DNA
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Matches
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Best Local
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OTHER INFORMATION: /mod_b
OTHER INFORMATION: /label
OTHER INFORMATION: /note-
FEATURE:
NAME/KEY: modified_base
ICCATION: 3538
OTHER INFORMATION: /mod_b
OTHER INFORMATION: /label
OTHER INFORMATION: /note-
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                                                                                                                 cttgtacccattggcaagtgttcctgcaatgctggctatgaagaaggaggttttatgtgc 657
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456; Conserva
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/label= N
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/label= N
/note= "Whe:
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Pred. No. 4.1e-96;
"*smatches 203;
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Sequence 102, Application US/08469537A
Patent No. 5843749
GENERAL INFORMATION:
APPLICANT: Maisonpierre, et al.
TITLE OF INVENTION: EHK AND ROR TY

al.
ROR TYROSINE

TITLE OF INVENTION: KI
NUMBER OF SEQUENCES: 1.
CORRESPONDENCE ADDRESS:

KINASES: 107

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Best Local Similarity 68.5%;
Matches 454; Conservative
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PRIOR APPLICATION NUMBER: USSN 08/406,247
APPLICATION NUMBER: USSN 08/144,992
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 08/144,992
FILING DATE: 28-OCT-1993
APPLICATION NUMBER: USSN 07/736,559
FILING DATE: 26-JUL-1991
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
       1028
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Kempler, Ph.D., Gail M
REGISTRATION NUMBER: 32,143
REFERENCE/DOCKET NUMBER: REG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914-345-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: unkn
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                                                                                           ggggtgaaatttcgagagcatcagtttacaaagattgacaccattgcagctgatgaaagt 300
                                                                                                                                                                  gttttaggaacttgcaaggagacattcaacctgtactacatggagtctgatgatgatcat
                                                                                                                                                                                                                                      gctcagaagatttatgtggagctcaagttcactctacgagactgcaatagcattccattg
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                                                                                                                                                                                                                                                                                                                 aatgtcatggaccacagtcaaaaccaattggctgagaaccaaactgggtccccagggaactca
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TTCACCGAACTTGACCTTGGAGACCGGGTCATGAAGCTGAATACGGAGGTCAGAGATGTA
                                                                                                                                              GGACTGGGGACTTGCAAGGAGACCTTTAACATGTATTATTTTGAGTCGGATGATGAGAAT 967
                                                                                                                                                                                                                   GCTTCCAGAATTTTTATTGAACTCAAGTTTACTCTGAGGGATTGCAACAGCCTTCCTGGA 907
                                                                     GGGAGAAATATCAAAGAGAACCAGTACATCAAGATCGATACCATTGCTGCTGATGAGAGC 1027
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Pred. No. 7.7e-95;
0; Mismatches 206;
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Query Match Best Local Similarity

48.1%;

Score 317.4; DB 2; Pred. No. 7.9e-95;

Length 4165;

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US-08-442-248-1
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US-08-442-248-1
                                                         TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELES: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4165 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1,
Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                  FILING DATE: 27-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: TOICH1a, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 920C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBERS
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                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/3
FILING DATE: 27-OCT-1994
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                            STRANDEDNESS:
                                           TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/442,248 FILING DATE: 15-MAY-1995
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RESULT 12
US-08-440-815-1
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patent No. 5798448
GENERAL INFORMATION:
APPLICANT: Caras, Ingrid W.
APPLICANT: Winslow, John W.
TITLE OF INVENTION: AL-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 Inch, 360 Kb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: path (Genentsch)
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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                                                                                                                                  ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno
CITY: South San Francisco
                                                                                                     COUNTRY:
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TELEPHONE: 415/225-8674
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4165 bases
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 454;
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FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/330128
FILING DATE: 27-OCT-1994
ATTORREY/AGENT INFORMATION:
NAME: TOICH14, Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 920C
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STRANDEDNESS: sing
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                  cttgtacccattggcaagtgttcctgcaatgctggctatgaagaagaggttttatgtgc
                                                                                              GTCAACCATTCTGTGACAGACGATCCTCCCAAAATGCATTGCAGTGCTGAAGGGGAGTGG
                                                                                                              gtcaacaattctaaggaggaagatcctccaaggaatgtactgcagtacagaaggcgaatgg
                                                                                                                                                                           CTGGTTTCTGTCCGTGTCTACTATAAAAAATGTCCTTCTGTAGTTAGACATTTGGCTGTT 1272
                                                                                                                                                                                                                                    ttggtgtctgtgagagtatacttcaaaaagtgcccatttacagtgaagaatctggctatg 480
                                                                                                                                                                                                                                                                              GGACCTCTGAGCAAAAAGGGATTTTATCTTGCTTTCCAAGATGTCGGTGCTTGCATCGCT
                                                                                                                                                                                                                                                                                               TTCACCGAACTTGACCTTGGAGACCGGGTCATGAAGCTGAATACGGAGGTCAGAGATGTA
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                                                                                                                                                        TTCCCTGACACGATCACTGGAGCAGATTCTTCCCAGTTGCTAGAGGTGTCAGGCTCCTGC
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            660
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US-08-673-789-1
                                                                                                                                                                                                                                                                                                               Matches 454;
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 4322
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TITLE OF INVENTION: BSK RECEPTOR LIKE TITLE OF INVENTION: TYROSINE KINASE AND LIG TITLE OF INVENTION: USE IN DIAGNOSTIC AND TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
TELEX: 421792
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MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/1:
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                       tgggaagagatcagtggtgtggatgaacattacacacccatcaggacttaccaggtgtgc 60
                                                         gttttaggaacttgcaaggagacattcaacctgtactacatggagtctgatgatgatcat 240
                                                                                                                                                                                         aatgtcatggaccacagtcaaaacaattggctgagaacaaactgggtccccaggaactca 120
ggggtgaaatttcgagagcatcagtttacaaagattgacaccattgcagctgatgaaagt 300
                                                                                                                                                                      AAAGTTATGGAACAGAATCAGAATAATTGGCTGTTGACCAGTTGGATCTCTAACGAAGGT 789
                                 GGACTGGGGACTTGTAAGGAGACATTTAACATGTATTATTTTGAATCAGATGATGAGAAT
                                                                                                    GCTTCCAGAATCTTTATTGAACTCAAGTTTACTTTAAGGGACTGCAACAGCCTTCCTGGA 849
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TYROSINE KINASE AND LIGAND AND THEIR
USE IN DIAGNOSTIC AND THERAPEUTIC
METHODS
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Pred. No. 8.1e-95;
0; Mismatches 206;
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RESULT 14
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US-08-449-645A-12
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                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION: APPLICANT: Fox, G
                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 10% CONTY: Thousand Oaks
STATE: California
                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 3162 base pairs
                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like
TITLE OF INVENTION: Kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1330 CAA 1332
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                                                  FEATURE:
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              NAME/KEY:
LOCATION:
                                                                                                                               LENGTH:
                                                                                                                                                                                                                                         CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                  TOPOLOGY:
                                                                                               STRANDEDNESS: single
                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Amgen Patent Operations/RBW STREET: 1840 Dehavilland Drive
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US-08-702-367A-12
US-08-702-367A-12
Sequence 12, Application US/0870236:
Patent No. 5981246
Patent No. 5981246
Patent INFORMATION:
APPLICANT: FOX, GAIY M.
TITLE OF INVENTION: EPH-Like Re
IITLE OF INVENTION: Kinases
UNMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 445; Conserv
ZIP: 91320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
OPERATING SYSTEM: PC-DOS,
                                                                                       ADDRESSEE: Amgen Pate
STREET: 1840 Dehavil!
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
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   compatible
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Pred. No. 3.8e-90;
                                                                                                                                                                                                                                     Receptor
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APPLICATION NUMBER: US/08,
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: 12.
INFORMATION FOR SEQ ID NO: 12.
SEQUENCE CHARACTERISTICS:
LENGTH: 3162 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
TOPOLOGY: linear
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Best Local Similarity
Matches 445; Conserv
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Search completed: May 15, 2000, 12:05:24 Job time: 4443 sec

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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Rat receptor tyros
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Mouse Bsk receptor
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EPH-like receptor
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Eph-related PTK Ce
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Protein tyrosine-k
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Claim 6; This sequence expressed tumours cand the (TK) and production analogues cellular Sequence	19-U 21-J 12-D (HALL Boyd Boyd WPI; P-PS Rece III- prot	mat_mat_ 07-J	SSULT 1 4513 Q34513 Q34513 Q34513 24-MAY Filmer eph/el ILila-1 TK; la-1 TK; la-1 TK; la-1 Synthe Key 5'utr cds 3'utr signal	33 35 35 36 37 37 37 37 37 37 37 37 37 37 37 37 37
Claim 6; Fig This sequence expressed in tumours of hu and the epith (TK) and/or i production an analogues hav cellular resp sequence 31	19-JUN-1992; AU 21-JUN-1991; AU 12-DEC-1991; AU ((HALL-) HALL IN BOYD AD, Simps WPI; 93-036373, P-PSDB; R31466. Receptor-type t RII-A4 - is EPH proteins in mod therapy etc.	_peptide _peptide _peptide _300425-A	LT 1 034513 standar 034513; 24-MAY-1993 (HEK coding seq Primer; expres eph/elk-like; Lila-l; JM; ep TK; ligand; B; Synthetic. Key 5'utr cds 3'utr signal_peptide misc feature	79.8 79.8 79.8 48.8 48.8 31.4 31.2
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ke kinase (HEK). HEK is	lkinson D; monoclonal antibody phosphorylating unction, in cancer	region"	n; human; HEK; lymphoid; LK63; hymidine kinase; rentiation; ss.	Human non-differen Receptor type tyro Coding sequence fo Receptor-type tyro EST clone CW960. N Human thymus receptor typ Human brain Expres Sequence used in d Non-inducible immu A. thaliana NIM-1

Query Match Best Local Similarity Matches 660; Conserv

100.0%; Score 660; DB 1; imilarity 100.0%; Pred. No. 1.4e-209; Conservative 0; Mismatches 0;

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08-UNT-1995.
07-SEP-1994; U10140.
03-DEC-1993; US-162809.
(LJOL-) LA JOLLA CANCER RE.
Pasquale EB, Sajjadi FG;
WPI; 95-215256/28.
P-PSDB; R75711.
                                                                                                                           Q90659 stand
Q90659;
11-NOV-1995
Eph-related
Cek4; Eph; p
prognosis; s
Gallus sp.
Disclosure; Page 85-89; 129pp; English.
Probes derived from the EPH-related PTKs Cek4 (090659) and (090660) were used to isolate novel cDNA clones (090652-58, 090661-62) from chicken embryo and embryonic brain librarie Cek4 is highly expressed in the chicken developing brain an
                             cancer.
Disclosure;
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Best Local S
Matches 537
W09528484-A1.
26-OCT-1995; U04681.
14-APR-1995; US-229509.
(AMGE-) AMGEN INC.
FOX GOT, Jung S. Welche
WPI; 95-373799/48.
P-PSDB; R85091.
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Local Similarity 81.4%;
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Prodn.

Prodn.

PS Claim 1; Page 57-62; 133pp; English.

CC cDNAs (702946-49) coding for 4 novel human EPH-like receptor protein

CC tyrosine kinases, HEKS, HEKF, HEKB and HEK11 (R85089-92), respectively,

CC were isolated from a human foetal brain cDNA library using a directed

CC Reproach with primers (see T02960-61) based on conserved regions of

CC receptor PTKs and EPH-like receptor PTKS. HEKF, HEKF, HEKF, and HEKB show

CC extensive homology to the catalytic domain of chicken EPH-like

CC receptors CekF, Cek7 and Cek8. HEK11 shows no homology to any known

CC EPH-like receptor. The isolated cDNAs are used for prodn. of

CC recombinant HEKS and chimeric receptors, in hybridisation assays, and

CC detect abnormalities in HEK receptor genes.

Sequence 3116 BP; 859 A; 720 C; 812 G; 725 T;
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Disclosure; Page 88-92; 125pp; English.

Disclosure; Page 88-92; 125pp; English.

Disclosure; Page 88-92; 125pp; English.

C DNA probes based on protein tyrosine-kinase (pTK) sequences were used to screen cDNA libraries to identify novel pTK genes. The bpTKs, bpTK1, bpTK2, bpTK3, bpTK4, bpTK5 and bpTK7 (R8924-28 and R85935, respectively) are expressed in human brain tissue and show homology to known pTKs. A full-length sequence for the bpTK7 gene (T03100) was obtd. This gene may be used to design new drugs, peptides and antisense constructs that modulate pTK activity.

Sequence 3348 BP; 924 A; 769 C; 855 G; 800 T;
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Best Local S
Matches 460
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04-APR-1994; US-222616.
(GETH ) GENENTECH INC.
Bennett BD, Goeddel D,
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WPI; 95-366160/47.
P-PSDB; R85936.
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01-DEC-1998.
06-JUN-1995; US-406247.
17-MAR-1995; US-406247.
26-JUL-1991; US-736559.
28-CCT-1993; US-144992.
06-JUN-1995; US-469537.
(RECE-) RECENERON PHARM INC.
Maisonplerre PC, Masiakowski P
WPI; 99-044884/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             V70208
V70208;
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The present invention describes nucleic acid molecules for ror-1, ror-2, ehk-1 and ehk-2. And ebk-2 the proteins are orphan receptor tyrosine kinases. The present sequence encodes rat Ehk-2. Sequence 3592 BP; 946 A; 916 C; 894 G; 834 T;
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01-DEC-1998.
06-JUN-1995; 469537.
17-MAR-1995; US-406247.
26-JUL-1991; US-736559.
28-OCTT1993; US-144992.
06-JUN-1995; US-449537.
(REGE-) REGENERON PHARM INC.
MAISONDIETTE PC, MASIAKOWSKI P
WPF; 99-044584/04.
P-PSDB; W83147.
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Rat receptor tyrosine kinase Ehk-1 encoding [
Receptor tyrosine kinase, Ror-1; Ror-2; Ehk-1
neurotrophin activity; trkB; proto-oncogene;
binding protein; BDNF; NT-3; diagnosis; ss.
                                                                                                                                                          The present invention describes nucleic acid molecules for ror-1 ror-2, ehk-1 and ehk-2. Also described are the corresponding pro Ror-1; Ror-2; Ehk-1; and Ehk-2. The proteins are orphan receptor tyrosine kinases. The present sequence encodes rat Ehk-1. Sequence 3906 BP; 1097 A; 876 C; 990 G; 943 T;
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09-MAY-1996.
26-OCT-1995; U14016.
27-OCT-1994; US-330118.
07-JUN-1995; US-486449.
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T18893;
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Sexample 1; Page 47-49; 75pp; English.

A cDNA clone (T18893) codes for rat REK7 (R97853), an eph-related tyrosine kinase receptor, for which AL-1 (see also w97854) is a ligand. It was isolated using degenerate receptor tyrosine kinase primers (T18894-96) to amplify cDNAs of an adult mouse hippocampal cDNA library. A PCR fragment was used as a probe to isolate the full-length REK7 cDNA from a rat hippocampal LDNA library. An REK-1gg fusion was used to screen cultured cell lines for surface expression of REK7-binding activity. Primers based on isolated ligands were used to amplify human breast carcinoma BT20 cell cDNA, and an amplified fragment was used to screen a human foetal brain cDNA library, leading to the isolation of AL-1 CDNA (T18897). Sequence 4165 BP; 1157 A; 907 C; 1035 G; 1066 T;
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Pred. No. 1.7e-95;
0; Mismatches 206;
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RESULT V58192 ID V5

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V58192 standard;

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PT with disease

PS Claim 2; Fig 2; 72pp; English.

CC The present sequence encodes mouse Bsk, which is a receptor-like

CC Typosine kinase. The nucleic acid sequence encoding Bsk can be used in

CC typosine kinase. The nucleic acid sequence encoding Bsk can be used in

CC trom a manmal selected with a disease, such as neurodegenerative

CC diseases or disorders and neoplasms. The nucleic acid sequence can also

CC be delivered into the limbic system of patients with limbic system

CC neurodegenerative disease, disorder or injury, to promote or enhance

CC diseases include, chromosomal abnormalities, degenerative growth and

CC development disorders, viral infections, bacterial infections, brain

CC injuries, neoplastic conditions, Alzheimer's disease, epilepsy,

CC schizophrenia, or stroke and cerebral ischaemia.

SQ Sequence 4322 BP; 1260 A; 887 C; 1055 G; 1120 T;
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Best Local Sim
Matches 454;
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29-SEP-1998.
11-JUN-1996; 673789.
04-JAN-1994; US-177812.
11-JUN-1996; US-673789.
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CDS
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Mouse Bsk receptor-like tyrosine kinase cDNA clone.
Mouse; Bsk; receptor-like tyrosine kinase; brain; diagnosis; neopla:
Mouse; Bsk; receptor-like tyrosine kinase; brain; diagnosis; neopla:
neurodegenerative disease; limbic system neuron regeneration;
chromosomal abnormality; degenerative growth; development disorder;
viral infection; bacterial infection; Alzheimer's disease; epilepsy
schizophrenia; stroke; cerebral ischaemia; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid sequence encoding protein - used in Bsk nucleic acid probes, used in detecting alterations in level of Bsk messenger-RNA in biological samples isolated from mammal afflicted
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Kromer LF, Schulz NT, Woude WPI; 98-541751/46.
P-PSDB; W71628.
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(SCHU/) SCHULZ N T.
(WOUD/) WOUDE G F V.
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418. .3051
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Pred. No. 1.7e
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TGGGAAGAGTTGGTGAAGTGGATGAAAATTATGCCCCTATCCACACATACCAAGTATGC

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 Query Match
Best Local S
Matches 445
                                                                     Claim 1; Page 49-54; 133pp; English.

CDNAS (T02946-49) coding for 4 novel human EPH-like receptor protein tyrosine kinases, HEK5, HEK7, HEK8 and HEK11 (R85089-92), respectively, were isolated from a human foetal brain cDNA library using a directed PCR approach with primers (see T02960-61) based on conserved regions of receptor PTKs and EPH-like receptor PTKs. HEK5, HEK7 and HEK8 show extensive homology to the catalytic domain of chicken EPH-like receptor. The isolated cDNAs are used for prodn. of recombinant HEKs and chimeric receptors, in hybridisation assays, and to detect abnormalities in HEK receptor genes.

Sequence 3162 BP; 921 A; 667 C; 775 G; 799 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T02947 standard; cDNA; 316
T02947;
16-APR-1996 (first entry)
                                                                                                                                                                                                                                                                   New nucleic acid encoding EPH-like receptor tyrosine kinase(s) and related vectors, host cells, proteins, antibodies etc., used diagnostically and therapeutically to modulate receptor activation
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WPI; 95
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Key
cds
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L5-APR-1994; US-229509
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   445;
h 45.9%;
Similarity 67.1%;
45; Conservative
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Score 303; DB 1;
Pred. No. 9e-91;
0; Mismatches 215;
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Gaps
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26-OCT-1995.
14-APR-1995; U04681.
15-APR-1994; US-229509.
(AMGE-) AMGEN INC.
FOX GM, Jing S, Welcher A
WPI; 95-373799/48.
      or prodn.

Claim 1; Page 66-71; 133pp; English.

cDNAs (T02946-49) coding for 4 novel

tyrosine kinases, HEK5, HEK7, HEK8 a

were isolated from a human foetal br
                                                                                                                                                             P-PSDB; R85092.

New nucleic acid encoding EPH-like receptor tyrosine kinase(s) and related vectors, host cells, proteins, antibodies etc., used diagnostically and therapeutically to modulate receptor activation
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T02949;
16-APR-1996 (first entry)
EPH-11ke receptor protein tyrosine
EPH-11ke receptor protein tyrosine
human eph-11ke kinase; therapy; dia
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Mouse developmental kinase 1 MDK1 T2 clone.

Mouse developmental kinase 1; MDK1 T2; receptor tyrosine RTK; signal transduction; probe; diagnosis; gene therapy; neurodegeneration; neuroproliferation; cancer; ss.

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T32962;
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Sequence 4529 BP; 1449 A; 834 C; 1000 G; 1246 T;
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Clossek T, Millauer B,
WPI; 96-333988/33.
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Example 1: Page 115-116; 128pp; English.

CDNA cloning using adult mouse brains and Northern blotting identified 2 clones, MDK1 T1 (T32961) and MDK1 T2 (T32962), that coded for truncated versions (W03422 and W03423; respectively) of the novel mouse developmental kinase 1 (MDK1) (see also T32960), a new member of the eck/eph family of receptor tyrosine kinases.

MDK T1 and T2 each possess the entire ectodomain, the transmembrane domain and part of the juxtamembrane region of MDK1 (see also W03421), but lack the catalytic tyrosine kinase domain. They may have a modulatory function. The cDNA clones can be used to produce MDK1

T1 and T2, which are useful for screening potential agents for treatment of diseases characterised by abnormal signal transduction. Sequence 2323 BP; 680 A; 497 C; 609 G; 537 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnosis and treatment
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P-PSDB; W03423.
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Query Match
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Example 1; Page 111-12; 128pp; English.

CDNA cloning using adult mouse brains and Northern blotting identified 2 clones, MDK1 T1 (T32961) and MDK1 T2 (T32962), that coded for truncated versions (W03422 and W03423, respectively) of the novel mouse developmental kinase 1 (MDK1) (see also T32960), a new member of the eck/eph family of receptor tyrosine kinases.

MDK T1 and T2 each possess the entire ectodomain, the transmembrane domain and part of the juxtamembrane region of MDK1 (see also W03421), but lack the catalytic tyrosine kinase domain. They may have a modulatory function. The cDNA clones can be used to produce MDK1 T1 and T2, which are useful for screening potential agents for treatment of diseases characterised by abnormal signal transduction. Sequence 2901 BP; 890 A; 578 C; 650 G; 783 T;
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Mouse developmental kinase 1; MDK1 T1 clone.
Mouse developmental kinase 1; MDK1 T1; receptor
RTK; signal transduction; probe; diagnosis; ger
neurodegeneration; neuroproliferation; cancer;
                                                                                                                                                                                                 New mouse development kinase 1 gene - used for developing prods diagnosis and treatment of abnormalities in signal transduction
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RESULT
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11-NOV-1996 (first entry)
Mouse developmental kinase 1 cDNA.
Mouse developmental kinase 1; MDK1; receptor tyrosine kinase;
signal transduction; probe; diagnosis; gene therapy;
signal transduction; neuroproliferation; cancer; ss.
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03-JAN-1996; U00419.
03-JAN-1995; US-368776.
(PLAC ) MAX PLANCK GES F
(SUGE-) SUGEN INC.
Clossek T, Millauer B,
WPI; 96-33398B/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A cDNA clone (T32960) codes for mouse developmental kinase 1 (MDK1) (W03421), a new member of the eck/eph family of receptor tyrosine kinases (RTKS): To isolate the clone, CDNA from mouse embryos was subjected to PCR amplification with primers based on conserved motifs (see also W03426-27) of RTKs. An amplified fragment was used to screen an 11.5-day-old mouse embryo and an adult mouse brain CDNA library to obtain the MDK1 clone. 4 Sequence variants (see also W03422-25) of MDK1 were also identified. MDK1 nucleic acids can be used for the recombinant prodn. of MDK1, as probes to detect MDK1, and for the gene therapy of diseases involving abnormalities in signal transduction, such as neurodegenerative and neuroproliferative disorders and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New mouse development kinase 1 gene - used for developing prods. diagnosis and treatment of abnormalities in signal transduction
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Pred. No. 4.2e-89;
0; Mismatches 208;
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Best Local Similarity
Matches 356; Conser
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Gallus sn
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08-JUN-1995: U10140.
07-SEP-1994: U10140.
03-DEC-1993: US-162809.
(LJOL-) LA JOLLA CANCER RE.
Pasquale EB, Sajjadi FG;
WPI: 95-215256/28.
P-PSDB: R75714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       variant Cek7+ (Q90661) were isolated from a chick embryo library in lambda gill, and another variant, Cek7' (Q90662), from a chick embryonic brain cDNA library in lambda gill. The variants may originate via alternative splicing of the same gene. Cek7 had the lowest level of expression of 7 novel Eph-related kinases examined and was barely detectable in adult tissues.

Sequence 3056 BP; 871 A; 661 C; 762 G; 767 T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer.
Claim 2; Page 106-109; 129pp; English.
Novel EPH-related PTK CDNA clone Cek7
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GCAGATTCCTCGCAGCTGCTAGAAGTGTCAGGCGTCTGTGTCAACCACTCAGTGACTGAT
                                                                                   TACAAGAAATGCCCATCAGTGATCCGCAACCTGGCACGCTTTCCAGATACCATCACAGGA
                                                                                                            ttcaaaaagtgcccatttacagtgaagaatctggctatgtttccagacacggtacccatg
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                       gactcccagtccctggtggaggttagagggtcttgtgtcaacaattctaaggaggaa
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Pred. No. 1.5e-71;
0; Mismatches 163;
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08-70W-1995:
07-SEP-1994: U10140.
03-DEC-1993: US-162809.
(LJOL-) LA JOLLA CANCER RE
PASQUATE EB, SAJJAGI FG:
WPI: 95-215256/28.
P-PSDB: R75705.
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Cek7; Eph; protein tyrosine-kinase; prognosis; ss.
Gallus sp.
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Sequence 3059 BP; 860 A; 632 C; 758 G; 809 T;
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11-NOV-1995
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                                                                                                             ttcaaaaagtgcccatttacagtgaagaatctggctatgtttccagacacggtacccatg
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                                                                                   TACAAGAAATGCCCATCAGTGATCCGCAACCTGGCACGCTTTCCAGATACCATCACAGGA
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Pred. No. 1.5e-71;
D; Mismatches 163;
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Perfect score:
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Maximum
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Copyright (c) 1993 - 2000 Compugen
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57: gb_htg12:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. a G ი Score Query Match Length 3149 3241 3254 3254 3254 3254 3254 3254 3254 3254 3254 3355 3355 BB 12 MMKIN1 4 DRAJ5030 12 RNU21955 12 RNU21954 4 GGY14271 4 XLSEK1 4 XELPAGAAA 10 HUMRPTKB 10 HSEHK1 10 HSEHK1 41 AC009425 10 HUMRPTK 32 HSJ189K14 32 HSJ189K14 444 12 5 5 5 2 4 5 HUMHEK RNU69278 RNU69278 MUSMEK4SE MUSMEK4 CHKCEK4 CHKCEK4 I15007 CHKCEK8 MMSEK MMSEK) HUMRPTKC 144522 AR062743 5 AC021499 5 RNEHK1 AR062744 AR025488 AR043381 2 MMU07357 GGCEK7B MMU72207 DRU89295) HS61A9 115010 115001 115009 5 AC023783 GGCEK8A IJ AC009425 HUMRPTK HSJ189K14 MMKIN1T2 MMKIN1T1 MMU58332 U90093 144522 Sequence 34 AR062743 Sequence AC021499 Homo sapi X78699 R. norvegicu AR062744 Sequence AR025488 Sequence AR043381 Sequence AR043381 Sequence U07357 Mus musculu X91191 X. laevis mR L26099 Xenopus lae L36644 Homo sapien X95425 H. sapiens m AC009425 Homo sapi L36642 Homo sapi L30694 M. musculus X79083 M. musculus X79083 M. musculus X79084 M. musculus X79085 Danio rer U21954 Rattus norv Y14271 Gailus 9all U03910 Gailus 9all U03910 Gailus 9all U03910 Gailus 9all U03910 Sequence 3 115001 Sequence 3 115001 Sequence 3 115001 Sequence 3 115009 Sequence 3 115009 Sequence 3 069278 Rattus norv M68515 Mouse ephr M68514 Chicken eph 115007 Sequence 15 D38174 Gallus gall X65138 M.musculus X551188 Sek-Eph-rel U58322 Mus musculu U90093 Human Chrom L36645 Homo sapien A28003 H.sapiens H I68018 Sequence 9 M83941 Human recep Description

ALIGNMENTS

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Primates; Catarrhini; Hominidae; Homo.
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Boyd, A.W., Simpson, R. John, Wicks, I.,
Method of screening for ligands to a
Patent: US 5674691-A 9 07-OCT-1997;
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3149)
Wicks,I.P., Wilkinson,D., Salvaris,E. and Boyd,A.W.
Molecular cloning of HEK, the gene encoding a receptor
kinase expressed by human lymphoid tumor cell lines
proc. Natl. Acad. Sci. U.S.A. 89 (5), 1611-1615 (1992)
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Homo sapiens lymphoid tumor cDNA to mRNA.
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                                       /COGON_Start=1
//COGON_Start=1
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receptor tyrosine
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101. .3052
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/tissue_type="lymphoid tumor"
101. .3052
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l. .3149
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/db_xref="taxon:9606"
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Best Local Similarity
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                                                                                  Eukaryota; Metazoa; Ch
Eutheria; Rodentia; Sc
1 (bases 1 to 3077)
L1,Y.Y., McTiernan,C.F
                                                                                                                                                                        U69278
U69278.1
2 (bases 1 to 3077)
Li,Y.Y., McTiernan,C.
Direct Submission
                                                                                                                                                                                            RNU69278 3077 bp
Rattus norvegicus eph:
(Rek4) mRNA, complete
                                            L1,Y.Y., McTiernan,C.F. and Feldman,A.M.
IL-1 beta alters the expression of the receptor gene r-EphA3 in neonatal rat cardiomyocytes
Am. J. Physiol. 274 (1), H331-H341 (1998)
                                     98120505
                                                                                                                                    Rattus norvegicus
                                                                                                                                                 Norway rat.
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Conservative (
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eph-related
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Pred. No. 4.7e-190;
           and
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           Feldman, A.M
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ae; Murinae;
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.nase homolog
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ttggtgtctgtgagagtatacttcaaaaagtgcccatttacagtgaagaatctggctatg
                                                               ggtcctgtcaacaagaagggattttattttggcatttcaagatgttggtgcttgtcttgcc
                                                                                                                                                  ttcactcaaatggatcttggggaccgtattctgaagctcaacactgagattagagaagta
                                                                                                                          TTCACTCAAATGGATCTCGGGGACCGCATTCTAAAACTCAACACTGAGATTAGAGAAGTG
                                                                                                                                                                                                           GGTGTCAAATTCCTAGAGCATCAGTTTACAAAGATTGACACCATTGCCGCTGATGAAAGT
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                                           GGACCAGTCAATAAAAAGGGGTTTTATTTGGCCTTTCAAGATGTTGGTGCTTGTTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 90.9
00; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  877
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FYKALDGVAKCTKCPPHSSTGEDGSMNCRCENNYFRAEKDPPSMACTRPPSARNVIS
NIMETSVILDWSWPLDTGGRKDITFNIICGENNYFRAEKDPPSMACTRPPSARNVIS
NIVETSVILDWSWPLDTGGRKDITFNIICGENVFURPERPGAGETNYT
TVTUDLLAHRINYTEEIDAINGVSELSSPPROFAAVSITINQAAPSPVMTIKKDRTSR
NSISLSWQEPEHPNGIILDYEVKYYEKQEQETSYTILRARGTNVTISSLKPDTTYVFQ
IRARTAAGYCTNSRKFEFENSPDSFSISGENSHVMIAISAARTIVLTVVTYVLVGR
FCGYTHAGYCTNSRKFEFENSPDSFSISGENSHVDTATAISAAVHEFAKNINAI
DKVVGAGEFGEVCSGRKLFENGHELFLPGLRTVPDDTYEEDAVAHEFAKNINGOFDHPN
IRLEGVVTKSKPVMIVTEYMENGSLDSFLRKHDAQFTVIQLVGMLRGIASGKKYLSD
IRLEGVVTKSKPVMIVTEYMENGSLDSFLRKHDAQFTVIQLVGMLRGIASGKKYLSD
IRLEGVVTKSKPVMIVTEYMENGSLDSFLRKHDAQFTVIQLVGMLRGIASGKKYLSD
IRLEGVVTKSKPVMIVTEYMENGSLDSFLRKHDAQFTVIQLVGMLRGIASGKKYLSD
IRLEGVVTKSKPVMIVTEYMENGSLDSFLRKHDAQFTVIQLVGMLRGIASGKKYLSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MDCHLSIIILFGCCVLSCSRELSPQPSNEVNLLDSKTIQGELGW
/SYPSHGWEEISGVDEHYTPIRTYQVCKVMDHSQNMLXTNWVPRNSAQKIYVELKFT
LRDCMSIPLYLGTCKETFILYYMSEDDDHGYKFLEHOFTKIDTIAADESFTQMDLGSKF
LKLNTEIREVGPVNKKGFYLAFQDVGACVALVSYRVYFKKCPFTVKNLAMFPDTVPM
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LMLDCWQKDRNNRPKFEQIVSILDKLIRNPGSLKIITSAAARPSNLLLLDQSNVDIATF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="eph-related receptor tyrosine kinase homolog"
/protein_id="AAC06273.1"
/db_xref="GI:1698722"
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35. .2989
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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/dev_stage="neonatal"
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/codon_start=1
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7.6e-161;
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polyA_site
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               1 tgggaagagatcagtggtgtggatgaacattacacaccccatcaggacttaccaggtgtgc 60
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                                                                al Similarity
595; Conserv
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1 (bases 1 to 2032)

Sajjadi.F.G., Pasquale,E.B. and Subramani,S.

Identification of a new eph-related receptor tyrosine kinase from mouse and chicken that is developmentally regulated and encodes at least two forms of the receptor

New Biol. 3, 769-778 (1991)
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Mouse eph-related
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rosine kinase.
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//db_xref="G1:454829"
//db_xref="G1:454829"
/ftanslation="ModHSILVILGCCVLSCSGELSPQPSNEVNLLDSKTIQGELGW
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IRDCNSIPLVLGTCKETFNLYYMESDDHGVKFREDGYFKIDITAADESSTQMDLGDRI
IKLNTEIREVEPPVNKKGFYLAFODVGACVALVSVRVYFKCPFTVKNLAMFDTFVFNL
IKLNTEIREVEPPVNKKGFYLAFODVGACVALVSVRVYFKCPFTVKNLAMFDTFVFND
SQSLVEVRGSCVNNSKEEDPPRNYCSTEGEWLVPIGKCTCNAGYEERGFICQACRPGF
YKASDGAAKCAKCPHSSTQEDGSMNCRCENNYFAABKDPPSNACARPPSAPRIVISN
INETSVILDMSWPLDTGGRKDITFNIICKKCGMNVRQCEPCSPNVRFLPRQLGITNTT
VTVTDLLAHTNYTFEIDAVNGVSELSSPPRQYAAVSITTNQAAPSPVMTIKKDRTSNI
SISLSWGEPEHPNGIILDYEVKYYQKOEGETSYTILRARGTNVTISSLKPDTTYVFQI
DASTACYCTMANDSFETERTGENCOWYGEF"
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/codon_start=1
/product="Mek4 secreted"
                                                                                                                                                                               RARTAAGYGTNSRKFEFETSPDCMYYFSF"
2010. .2015
2032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="IRC x Swiss Webster"
/db_xref="taxon:10090"
/dev_stage="11.5 day_embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_
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                                                            Score 544.8; DB 12
Pred. No. 5.2e-155;
0; Mismatches 62;
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
1 (bases 1 to 3197)
Sajjadi,F.G., Pasquale,E.B. and Subramani,S.
Identification of a new eph-related receptor tyrosine
from mouse and chicken that is developmentally regulat
encodes at least two forms of the receptor
New Biol. 3, 769-778 (1991)
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M68513.1 GI:199119
receptor tyrosine kinase.
Mus musculus (strain IRC:
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eph-related
                /gene="Mek4"
89. .3040
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                                                                                          Location/Qualifiers
1. .3197
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/codon_start=1
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receptor
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     GTCCCCATTGGCAAATGCACTTGCAATGCTGGGTATGAAGAACGAGGTTTCATATGCCAA
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/product="receptor tyrosine kinase"
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yaksdaakcakcpphesgroundstopspopsnevnllsslkpdtyvrgq
yaksdaakspopsnevnlldstandstanvalivitvvyvrycyggr
yaksdaakspopsilldysvkrygkoegetsytilaakgtmytisslkpdtyvrgqr
sislswoepenpengilldysvkrygkoegetsytilaakgtmytigakslagkkrysdb
kvygagefgevcsgrlklpskkeisvalktlkvgttekorrdflagaakslagkkrysdb
kvygagefgevcsgrlklpskkeisvalktlkvgttekorrdflagaakslagkkrysdb
kvygagefgevcsgrlklpskkeisvalktlkvgttekorrdflagaakslagkkrysdb
kvygagefgevcsgrlklpskkeisvalktlkpdkyttygptkopshocpaalyg
gyhrblaaknillinsklvckvsdefdskrylbopsayftrogklipslasgkkrysdb
gyhrblaarnillinsklvckvsdefdskrylbopsayftrogklipslasgkyth
gyhrblaarnillinsklvckvsdefdskrylbiakspaakspsklllogsnydlaffh
trogknordvpv"
grfsasdvaksfedivsildklinapgslkiitsaaarpsklllogsnydlaffh
ergsknordvpv"
767 c 775 g 748 t
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                         gctcagaagatttatgtggagctcaagttcactctacgagactgcaatagcattccattg 180
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Chicken eph-related receptor tyrosine kinas
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receptor tyrosine kinase.
Gallus gallus 10 day embryo embryo cDNA to
Gallus gallus
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Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
1 (bases 1 to 3241)
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                                                                                                                                                                                                                                                                                                                                                                                                                       /product="receptor tyrosine kinase"
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SQSLVEVRGSCVNHSKEEEPPKMYCSTEGEWLVPIGKCLCNAGYEERGFACQACRPGF
YKASAGNVKCAKCPEHSSTYEDASLNCRCEKNIFFSEXDPPSMACTRPPSAPRAVISN
INETSVILDWSWPLDTGGRKDVTFNIICKKCGGSKICEPCSDNVRFLPRQTGLINTT
VTVVDLLAHTNYTFEIDAVNGYSDLSFLSRQFAAVSITINGAAPSPITVTRORISN
SVSLSWGPEHENGILLDYEKYYEKQEGETSYTILFAAKSTNVTISGLKPDTTYVFQI
RARTAARYGTSSRKFEFTSPDSFSISSENGVVMIAISAAVAIILLTVVVYVLLGRF
CGYKKSKHGTDEKRLHERGHHLKLPGLETYVDPHTYEDORAVHEFAKELDASNISID
KVVGAGEFGEVCSGRIKLPSKKEISVAIKTLKAGYTEKQRRDFLGEASIMGOFDHPNI
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RKFTSASDAWYGGILJMEVMSYGERFYWEMSFODVIKAVDEGYKLPFPMDCPAALYQL
MLDCWGNDRNNRPKFEQIVSILDKLIRPSSLKIITNAAARPSNLLDQSNIDISAFR
TAGDWLNGFRTGQCKGIFTGVEYSSCDTIAKISTDDMKKVGVTVVGPQKKIVSSIKTL
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/codon_start=1
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/dev_stage="10 day embryo"
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I15007
I15007.1 GI
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Pasquale, E.B. and Sajjadi, F.G.
Eph-related tyrosine kinases,
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                                                                                                                                   Submitted (09-SEP-1994) to the DDBJ/EMBL/GenBank databases. Kunimasa Ohta, Kunamoto University Graduate School of Medical Sciences, Dept. of Neuroscience and Immunology; 4-24-1 Kuhonji, Kumamoto, Kumamoto 862, Japan (B-mail:ohta)203@gpo.kumamoto-u.ac.jp, Tel:096-344-2111(ex.6754
                                                                                                                                                                                                                                                                                                  Ohta, K., Nakamura, M., Hirokawa, K., Tanaka, S., Iwama, A., Suda, Ando, M. and Tanaka, H.
The receptor tyrosine kinase, Cek8, is transiently expressed
                                                                                                                                                                                                               Ohta, K.
                                                                                                                                                                                                                       Unpublished (1996)
3 (bases 1 to 3600)
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Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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  /codon_start=1
/product="Cek8"
/protein_id="BAA07373.1"
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                                                                                                               ocation/Qualifiers
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WIASPLEGGREEVS IMEEKNIP I ITYOCYCHVEEPSONNELRIUDSRSVQGELG
WIASPLEGGREEVS IMEEKNIP I RTYCOYCHVEEPSONNELRIWIP REGAORTY I EIK
FTLRDCNSLPGVMGTCKET FILLY Y ESHIDKERF I RESOFAKIDI I RADESTTOVDI G
DRIMKLNITEVROVGPLSKKGFYLAFQDVGACIALVSVRVFYKKCPLTVERLAGFEDTI
TGADI'SSLVEVRAGSCVINSEEKDVPKMYCGADGEMLVPI GNCLCHAGSTEERNGECOAC
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Charnay, P.
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Gilardi-Hebenstreit, P., Nieto, M.A., Frain, M., Ma
Chestler, A., Wilkinson, D.G. and Charnay, P.
An Eph-related receptor protein tyrosine kinase
expressed in the developing mouse hindbrain
Oncogene 7 (12), 2499-2506 (1992)
93096484
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M.musculus mRNA for tyrosine
X65138 S51422
X65138.1 GI:54083
Sek gene; Tyrosine kinase.
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103..3015
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S57168
S57168.1
l (bases 1 to 4242)
Gilard: Hebenstreit, P., Nieto, M.A., Frain, M.,
Chestier, A., Wilkinson, D.G. and Charnay, P.
                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

[ (bases 1 to 4242)
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Pred. No. 1.1e-89;
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                                                                              9999tgaaatttcgagagcatcagtttacaaagattgacaccattgcagctgatgaaagt
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TTCACGCAGGTGGACATTGGTGACCGAATCATGAAACTCAACACTGAGATCCGGGATGTA
                       ttcactcaaatggatcttggggaccgtattctgaagctcaacactgagattagagaagta 360
                                                                                                                                                            GTCATGGGGACTTGCAAGGAGACGTTTAACCTCTACTACTATGAGTCGGACAACGACAAG
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entry (NCBI gibbsq 127779) from the original journal article.
This sequence comes from Fig. 5.
*ERRATUM* Gilardi-Hebenstreit et al., Oncogene (1992)7, 2499-
Location/Qualifiers
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KIGYYKALSTDASCAKCPPHSYSVWEGATSCTCDRGFERADNDAASMPCTRPPSAPLN
LISWNETSVYLEWSSPQNTGGRODISYNVCKKCGAGDPSKCRPCGSGVHYTPQQNG
LKTTRVSITDLLAHTNYTFEIRAVNGVSKYNPSSPQSVSYTYTNQAAPSSIALVQAK
EVTRYSILLAHTNYTFEIRAVNGVSKYNPSSPQSVSYTYTNQAAPSSIALVQAK
EVTRYSILLAHTLATTTFEIRAVNGVSKYNPSSPQSVSYTYTNQAAPSSIALVQAK
EVTRYSVALAWLEPDRENGVILLEYEVKYYEKDQNERSYRLYRTAARNTDIKGLNPLTS
YVFHVRARTAAGYGDFSEPLEVTTNTVPSFRIIGDGRANSTVLLVSVSGSVVLVVILIAA
FVISRRSKYSKAKQEADEEKHLNGGVRTYDDFTYEDPRQAVREFAKEIDASCIKIE
KVIGVGEFGEVCSGRLKVPGKREICVAIKTLKAGYTDKQRADFISEASIMGQFDHRNI
IHLEGVYTKCKPYMIITEYMENGSLDAFIRKNDGFFTYTQLVGMLRGIGSGMKYLSDM
SYVHRDLAARNILTUNSHLVCKVSDFGMSRVLEDDPEAAYTTRGKRIFIRWRFAFAIAY
RKFTSASDVRSYGIIVMSHLVCKVSDFGMSRVLEDDPEAAYTTRGKRIFIRWRFAFAIAY
RKFTSASDVRSYGIIVMSHLVCKVSDFGMSRVLEDDPEAAYTTRGKRIFIRWRFAFAIAY
RKFTSASDVRSYGIIVMSHLVCKVSDFGMSRVLEDDPEAAYTTRGKRIFIRWRFAFAIAY
RKFTSASDVRSYGIIVMSTAGATTLEAVVHMSQDDLARIGITAITHQNKIISSVQAM
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FTLRDCNSLPGVMGTCKETFNLYYYESDNDKERFIRESQFGKTDTIAADESFTQVDIG
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*ERRATUM* Gilardi-Hebenstreit et al., Oncogene
2499-2507; This sequence comes from Fig. 5"
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U58332.1 GI:
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19104-6082, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lee, A.M., Navaratham, D., Ichimiya, S., Greene, M.I Cloning of m-ehk2 from the murine inner ear, an tyrosine kinase expressed in the developing and DNA Cell Biol. 15 (10), 817-825 (1996)
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, A.M., Ichimiya, S.,
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/translation="mggevrefildfrfflhiamtgdcshysnqvylldttvmg
Elgwktyflngwafitemdehnreihtyryckrymepronwilenwaferdagkiyve
Mketlrokus i pwylgteknreihtyryiesdeshgtkfkrokgyikidtaadesftomb
Lgdrilkinteirevgplerkgfylyyiesdeshgtkfkrokgykeirggs
Lgdrilkinteirevgplerkgfylyiesdeshgtkykyrokkcpptyrslamepd
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Acrofykeirggscyksaeerdfpklycgaddmilvplarcigstgyeeirgsch
Acrofykeirgscyksaeerdfpklycgaddmilvplarcdpsgadcireiprhf
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RNVAFNINETALILEWSPPSDTGGKKOLTYSVLCKKGGLDTTQCEDGGGLReiprhf
GLINNSVVLDFYSHVNYTEEIEAMNCVSELSISPKPTAITYTDHDAPSLIGMMRK
DMASQNSLLENGAAFSNGAILDYETKYYEKEBGJUTYSGTKAPSVITTGLKPAT
TYIFHIRVRTATGYSGYSGKFEFETGLETSDMAAEQGGILVISTRAAVGEFTLLVILT
DMASQNSLLENGAAFSNGAILDGETKYYEKEBGJUTYSDDDTYEDDSLAVHEFAKE
EFLITGROGWILKAKMKSEEKRRTHLONGHLRFPGIKTYIDDDTYEDDSLAVHEFAKE
                                                                                                                                                                                                                                    /product="receptor tyrosine kinase"
/protein_id="AAB53836.1"
/db_xref="GI:1457961"
                                                                                                                                                                                                                                                                                                                     /note="eph-related tyrosine kinase; simil
norvegicus receptor-like tyrosine kinase
Accession Number S51605"
                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus'
/strain="Balb/c"
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PAGRPVMIVVEYMENGSLDSFLRKHDGHFTVIQLVGMLRGIASGMKYLSDMGYVHRDL
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DAWSYGIVMWEVMSYGERPYWEMSNQDVILSIEEGYRLPAPMGCPPSLQQLMLHCWQK
ERNHRPKFTDIVSFLDKLIRNESALHTLVEDILVMPESPGDVEEYPLFVTVGGWLDSI
KMGQYKSNFMAAGFTTFDLISRMSIDDIRRIGVILIGHQRRIVSSIQTLRHMMHIQE
KGFHV"
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Direct Submission

Submitted (14-FEB-1997) Informatics, Southwestern Medical Center,

5323 Harry Hines, Dallas, TX 75235-8591, USA

3 (bases 1 to 77197)

Evans,G.A., Bradbury,P., Brignac,S., Bumeister,R., Burbee,D.,

Davie,J., Davies,C.J., Davis,C., English,C., Fondon,T.,

Franklin,T.L., Garner,H.R., Gordon,M., Gotway,G., Grant,O.,

Hahner,L., Harris,J., Hinson,S., Megarity,C., Narayanaswamy,U.,

Newton,J., O'Brien,K., Oliver,T., Patel,P., Probst,S., Rayner,S.,

Schageman,J., Schilling,P., Schultz,R., Syed,M., Valenzuela,D.,

Ward,T. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (06-AUG-1997) Genome Science and Technology Center,
University of Texas Southwestern Medical Center at Dallas, 53
Harry Hines Blvd, Dallas, TX 75235-8591, USA
On Jun 19, 1997 this sequence version replaced gi:1890102.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Franklin,T.L., Garner,H.R., Gordon,M., Gotway,G., Grant,O., Hahner,L., Harris,J., Hinson,S., Megarity,C., Narayanaswamy,U., Newton,J., O'Brien,K., Oliver,T., Patel,P., Probst,S., Rayner,S., Schageman,J., Schilling,P., Schultz,R., Syed,M., Valenzuela,D., Ward,T. and Wilson,R.
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1 (Dases 1 to 77197)

Evans,G.A., Bradbury,P., Brignac,S., Bumeister,R., Burbee,D., Bavie,J., Davies,C.J., Davis,C., English,C., Fondon,T., Ersellis, T., Edge, C.J., Davis,C., English,C., Fondon,T., Fo
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/rpt_family="MER25"
complement(35627. .36
/rpt_family="LTR13"
complement(40418. .40
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/rpt_family="L1"
complement(25614.
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/db_xref="taxon:9606"
/clone="pDJ298k13"
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                                                                        tttccagacacggtaccca---tggactcccagtccctggtggaggttagaggggtcttgt
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GTGAAGAGTGCTGAAGAGCGTGACACTCCTAAACTGTATTGTGGAGCTGATGGAGATTGG
                    gtcaacaattctaaggaggaagatcctccaaggatgtactgcagtacagaaggcgaatgg 597
                                                                                                                  CTGGTTTCAGTCCGTGTTTTCTACAAGAAATGCCCCTTCACTGTTCGTAACTTGGCCATG
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Similarity 69.5%;
60; Conservative
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complement(69359.
/rpt_family="MIR"
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/rpt_family="Alu"
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1 (bases 1 to 3107)

Fox,G.M., Holst,P.L., Chute,H.T., Lindberg,R.A., Janssen,A.M., Basu,R. and Welcher,A.A.

CDNA cloning and tissue distribution of five human EPH-like receptor protein-tyrosine kinases
Oncogene 10 (5), 897-905 (1995)
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EPH-1ike receptor PTK; receptor protein-tyrosine kinase.
HOMO Sapiens (clone library: Stratagene premade library, cat
#936206) female fetus, 17-18 weeks gestation brain cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMRPTKC 3107 bp mRNA PRI 10-AUG-1995 Homo sapiens receptor protein-tyrosine kinase (HEK8) mRNA, con
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//codon_start=1
//protein_id="naceptor protein-tyrosine kinase"
//protein_id="naceptor protein-tyrosine"
//db_xref="gi:551614"
//dic_xref="gi:551614"
/
                                                             2995. .3107
/gene="HEK8"
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                                                                                                                                                                     MLDCWQKERSDRPKFGQIVNMLDKLIRNPNSLKRTGTESSRPNTALLDPSSPEFSAVV
SVGDWLQAIKMDRYKDNFTAAGYTTLEAVVHVNQEDLARIGITAITHQNKILSSVQAM
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34. .2994
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/tissue_type="brain"
1. .3107
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Bennett, B.D., Goeddel, D. and Matthews, W.
Protein tyrosine kinase agonist antibodies
Patent: US 5635177-A 34 03-JUN-1997;
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Search completed: May 15, Job time: 18656 sec 2000, 11:43:49

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Total number of hits satisfying chosen parameters:
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1: /cgn2_6/ptodata/;

2: /cgn2_6/ptodata/;

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Copyright (c) 1993 - 2000 Compugen
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PCT-US96-00419-5
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                  Sequence 10,
Sequence 21,
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Sequence 101,
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Sequence 20,
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e 16, Appl
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                  101 App
15, App1
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36, App1
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30, App
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30, App
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17, App
17, App
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627	632	632	632	644	644	681.5	681.5	681.5	693.5	708	708	708	713	713	715
52.2	52.7	52.7	52:7	53:7	53.7	56.8	56.8	56.8	57.8	59.0	59.0	59.0	59.4	59.4	59.6
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US-08-449-645A-18	PCT-US95-04681-20	US-08-702-367A-20	US-08-449-645A-20	US-08-162-809-14	US-08-162-809-10	US-08-162-809-20	US-08-162-809-4	US-08-162-809-22	US-08-673-789-6	PCT-US95-04681-11	US-08-702-367A-11	US-08-449-645A-11	US-08-162-809-12	US-08-162-809-18	us-08-673-789-5
18	Sequence 20, Appl	Sequence 20, Appl	Sequence 20, Appl	Sequence 14, Appl	Sequence 10, Appl	Sequence 20, Appl	Sequence 4, Appli	Sequence 22, Appl	Sequence 6, Appli	1	Sequence 11, Appl	Sequence 11, Appl	Sequence 12, Appl	Sequence 18, Appl	Sequence 5, Appli

ALIGNMENTS

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US-08-167-919A-10
US-08-167-919A-10
Sequence 10, Application US/08167919A
Sequence 10, Application US/08167919A
Sequence 10, Application US/08167919A
Sequence 10, Sequence 1
Sequence 10, Application US/08167919A
APPLICANT: Simpson, Richard J.
APPLICANT: Simpson, Richard J.
APPLICANT: Simpson, Richard J.
APPLICANT: Wicks, Ian
APPLICANT: Wicks, Ian
APPLICANT: Wicks, Ian
APPLICANT: Wilkinson, David
TITLE OF INVENTION: AN USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE; SCULLY, SCOTT, MUTPHY & Presser
STREET: 400 Garden City
STATE: New York
COUNTRY: U.S.A.
INFORMATION TYPE: Ploppy disk
COUNTRY: U.S.A.
INFORMATION TYPE: Ploppy disk
COMPUTER: BABABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: BAPLICATION NUMBER: US/08/167,919A
CLASSIFICATION NUMBER: US/08/167,919A
FILING DATE: 18-APP-1994
CLASSIFICATION NUMBER: US/08/167,919A
FILING DATE: 12-UN-1991
PRIOR APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION NATA:
APPLICATION NUMBER: PK992 (AU)
FILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU92/00294
FILING DATE: 19-JUN-1992
ATTORNEY/AGREM INFORMATION:
TELEPRNIC JOCKET NUMBER: 9159
TELECOMMUNICATION OF SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acids
TOPOLOGY: 11near
MOLECULE TYPE: mino acids
TYPE: amino acids
TYPE: amino acids
TYPE: mino acids
TYPE: mino acids
TYPE: processore
TYPE: mino acids
TYPE: processore
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                                                                                                                             Query Match
Best Local S
Matches 220
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GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 21:
                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATECHIN Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/449,645A
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
      112
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hes 220;
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              61 VLGTCKETFNLYYMESDDDHGVKFREHOFTKIDTIAADESFTQMDLGDRILKLNTEIREV 120
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                                                                                                                                                                                                                                                                   TYPE: amino acid
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                                                         WEEISGYDEHYTPIRTYQYCNYMDHSQNNWLRTNWYPRNSAQKIYYELKFTLRDCNSIPL 111
                                                                              WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL 60
VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV
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                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                   single
                                                                                                                                        100.0%; Score 1200; DB 2; 100.0%; Pred. No. 3.7e-122;
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Pred. No. 3.7e-122;
                                                                                                                           Mismatches
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RESULT 4
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; Sequence 10, Application US/08715106
; Patent No. 6020306
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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-702-367A-21
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Best Local Similarity
Matches 220; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,367A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         172
                                                                                                                            181 NNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ 220
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                                                                                                                                                                                                121 GPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCV 180
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CLASSIFICATION: 435
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ZIP: 91320
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STATE: California
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5. 5981246
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40 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1200; DB 2; 100.0%; Pred. No. 3.7e-122; tive 0; Mismatches 0;
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Best Local
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FILING DATE: 18-APR-1994
APPLICATION NUMBER: PK6841 (AU)
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PK9992 (AU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PK9992
FILING DATE: 12-DEC-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU
FILING DATE: 19-JUN-1992
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9159
TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 983 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: UFILING DATE: 18-SEP-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wilkinson, David
TITLE OF INVENTION: A NOVEL RECEPTOR-TYPE TYROSINE KINASE
TITLE OF INVENTION: AND USE THEREOF
NUMBER OF SEQUENCES: 14
                                                              112 VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV
                181 NNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ 220
                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Scully, Scott, Murphy & Presser STREET: 400 Garden City Plaza CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: DiGiglio, Frank S. REGISTRATION NUMBER: 31,
                                                                                                                                                     VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV 120
NNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ 271
                                                                                                                                                                                                                                                                                                Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                        983 amino acids
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                                                                                                                                                                                                                                                                             100.0%; Score 1200; DB 3; ilarity 100.0%; Pred. No. 3.7e-122; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-SEP-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PCT/AU92/00294
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                                                                                                                                                                                                                                                                                                            Length 983;
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                                                                                                                               Sequence 16, Application US/08162809 Patent No. 5457048 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 220; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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TOPOLOGY: line
MOLECULE TYPE: F
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04681
                                NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                               APPLICANT: Pasquale, Elena B.
APPLICANT: Sajjadi, Foreydoun G.
TITLE OF INVENTION: NOVEL EPH-RELATED TYROSINE KINASES,
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES, AND METHODS (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Fox, Gary M
                                                                                                                                                                                                                                                                                                                                                                           232
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                                                                                                                                                                                                                                                                                                                   172
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STREET: 4370 La
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
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                                                                                                                                                                                                                                                                   NNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ 220
                                                                                                                                                                                                                                                                                                                                GPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCV 180
                                                                                                                                                                                                                                                NNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ 271
                                                                                                                                                                                                                                                                                                               GPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCV
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California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 1200; DB 4; ilarity 100.0%; Pred. No. 3.7e-122; Conservative 0; Mismatches 0;
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                 CAMPBELL AND FLORES
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 Jolla Village Drive,
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 Suite 700
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                                                               OF USE
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LENGTH: 983 millio acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-162-809-16
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                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: ZHOU, RENPING
APPLICANT: T; KROMER, L
APPLICANT: GEORGE, F.
TITLE OF INVENTION: BSK
TITLE OF INVENTION: TYRO
TITLE OF INVENTION: WISE
TITLE OF INVENTION: WISE
TITLE OF INVENTION: WISH
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08673789 Patent No. 5814479
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                COUNTRY: US
ZIP: 10154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 WEEISGVDEHYTPIRTYQESNVMDHSQNNWLRTNWIPRNSAQKIYVELKFTLRDCNSIPL 110
                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL
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                                                                                                                    NEW YORK
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C: United States
                                                                                                                                                          345 PARK AVENUE
                                                                                                  USA
                                                                                                                                                                                                                                                                                                                               ZHOU, RENPING; SCHULZ, NICHOLAS,
T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
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                                                                                                                                                                              MORGAN & FINNEGAN
                                                                                                                                                                                                                                TYROSINE KINASE AND LIGAND AND THEIR USE IN DIAGNOSTIC AND THERAPEUTIC METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94.7%;
94.1%;
                                                                                                                                                                                                                                                                                             BSK RECEPTOR LIKE
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Pred. No. 3.5e-115;
7; Mismatches 6;
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APPLICANT: ZHOU, RI
APPLICANT: T.; KROI
APPLICANT: GEORGE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/08673789 Patent No. 5814479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local Similarity 94.1%;
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                                                                                                                                                                                                                                                               TITLE OF INVENTION: BSK RECEPTOR LIKE
TITLE OF INVENTION: TYROSINE KINASE AND LIGAND AND THEIR
TITLE OF INVENTION: USE IN DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAX: (212) 751-6849
TELEFX. 421707
                                                                                         ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/17
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 982
                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 NNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 VLGTCKETFNLYYMESDDDHLAKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEVREV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 GPVSKKGEYLAFODVGACVALVSVRVYFKKCPFTVKNLAMFPDTVPMDSQSLVEVRGSCV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: AMINO ACID
STRANDEDNESS: UNI
                                   COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WORDPERFECT 5.1
                                                                                                                                      COUNTRY: UZIP: 10154
                                                                                                                                                                            CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                     STREET:
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                                                                                                                                                                                                                                      ADDRESSEE:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NHSKEEEPPKMYCSTEGEWLVPIGKCLCNAGYEERGFACQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207;
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                                                                                                                                                                                                                     345 PARK AVENUE
                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                               ZHOU, RENPING; SCHULZ, NICHOLAS,
T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
                                                                                                                                                                                                                                                                                                                                                                               GEORGE, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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  us/08/673,789
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Pred. No. 9.5e-115;
7; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 982;
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CLASSIFICATION:

08/177,812

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US-08-469-537A-101
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REFERENCE/DOCKET NUMBER: 2026
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEPAS: (212) 751-6849
TELER: 421792
INFORMATION FOR SEQ ID NO: 3:
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Best Local s
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 101, Application US/08469537A Patent No. 5843749
SOFTWARE: FastSEO Version 2.0
CURRENT APPLICATION DATA:
APPLICATION UNMER: US/08/469,537A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/406,247
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: USSN 08/144,992
FILING DATE: 28-OCT-1993
                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/1
FILING DATE: 04-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 VNNSEEKDVPKMYCGADGEWLVPIGNCLCNAGYEERGFACQ 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 VNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
                                                                                                                                                                                                                                                                                 STREET: 777 Old
CITY: Tarrytown
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nes 164; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: AMINO ACID
STRANDEDNESS: UNK
TOPOLOGY: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV 120
                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                     ADDRESSEE: Regeneron Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPLSKKGFYLAFQDVGACIALVSVRVFYKKCPLTVRNLAQFPDTITGADTSSLVEVRGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSC
                                                                                                                                                                                                                                          10591
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                                                                                                                                                                                                                                                                                                                                                                         Maisonpierre, et al.
VENTION: EHK AND ROR TYROSINE
VENTION: KINASES
                                                                                                                                                                                                                                                        U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76.5%; Score 917.5; DB 2; 74.2%; Pred. No. 2.2e-91; tive 28; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                             107
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US-08-449-645A-15
; Sequence 15, Application US/08449645A
; Patent No. 5981245
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SEQUENCE CHARACTERISTICS:
LENGTH: 948 amino acids
                                REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 914-345-7400
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NAME: Kempler, Ph.D., Ga
                                                                                        ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Pat
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 VNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      176 GPIERKGFYLAFQDIGACIALVSVRVFYKKCPFTVRNLAMFPDTIPRVDSSSLVEVRGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 YLGTCKETFTLYYIESDESHGTKFKPSQYIKIDTIAADESFTQMDLGDRILKLNTEVREV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          236 VKSSEERDTPKLYCGADGDWLVPLGRCICTTGYEE
                                                                                                                              FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                            STREET: 1840 Dehavi:
CITY: Thousand Oaks
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56 WDAITEMDEHNRPIHTYQVCNVMEPNQNNWLRTNWISRDAAQKIYVEMKFTLRDCNSIPW 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76.2%; Score 914.5; DB 2
Local Similarity 74.0%; Pred. No. 4.4e-91;
les 159; Conservative 31; Mismatches 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Kempler, Ph.D., Gail I REGISTRATION NUMBER: 32,143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 WEEISGYDEHYTPIRTYQYCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL
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amino acid
            986 amino acids
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26-JUL-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
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114 VMGTCKETFNLYYYESDNDKERFIRENQFVKIDTIAADESFTQVDIGDRIMKLNTEIRDV

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                                                                                                                                                                                                ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: prot
US-08-702-367A-15
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US-08-702-367A-15
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Best Local
                                                                                                                        Matches
                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: A INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS: LENGTH: 986 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: Fox, G
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 10% CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: EPH-Lik
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174
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                                  61
                                                              54
                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54
                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL 60
                                                                         WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WEEVSIMDEKNTPIRTYQVCNVMEPSQNNWLRTDWITREGAQRVYIEIKFTLRDCNSLPG 113
                             VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV 120
                                                           WEEVSIMDEKNTPIRTYQVCNVMEPSQNNWLRTDWITREGAQRVYIEIKFTLRDCNSLPG 113
                                                                                                                        162;
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1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fox, Gary M.
                                                                                                                     75.5%; Score 905.5; llarity 73.3%; Pred. No. 4.5. Conservative 30; Mismatches
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                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
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73.3%;
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            4.5e-90;
ches 28;
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                                                                                                                                                 Length
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       RESULT 13
US-08-222-616-36
US-08-222-616-36
; Sequence 36, Application U
; Patent No. 5635177
; GENERAL INFORMATION:
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PCT-US95-04681-15
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                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 986 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FOX, GARY M.
TITLE OF INVENTION: EPH-Like
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Winter, Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 184v CITY: Thousand Oaks
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Pat
                 180 VNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ
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 234
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                                                                                                                                                    61 VLGTCKETFNLYYMESDDDHGVKFREHOFTKIDTIAADESFTQMDLGDRILKLNTEIREV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                      54 WEEVSIMDEKNTPIRTYQVCNVMEPSQNNWLRTDWITREGAQRVYIEIKFTLRDCNSLPG 113
                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                         1 WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL
                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                   GPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSC
                                                                                                                                    VMGTCKETFNLYYYESDNDKERFIRENQFVKIDTIAADESFTQVDIGDRIMKLNTEIRDV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VNNSEEKDVPKMYCGADGEWLVPIGNCLCNAGHEERSGECQ
VNNSEEKDVPKMYCGADGEWLVPIGNCLCNAGHEERSGECQ
                                                                 GPLSKKGFYLAFQDVGACIALVSVRVFYKKCPLTVRNLAQFPDTITGADTSSLVEVRGSC
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Pred. No. 4.5e-90;
""" matches 28;
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US/08222616

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RESULT 14
PCT-US95-04228-36
; Sequence 36, Application PC/TUS9504228
; GENERAL INFORMATION:
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Best Local Similarity 73.3
Matches 162; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1104 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/826935 FILING DATE: 22-JAN-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US93/00586 FILING DATE: 22-JAN-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: WOOD, WILLIAM I.
TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST
TITLE OF INVENTION: ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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APPLICANT:
APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/25-1994
TELEFAX: 415/952-9881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: 5.25 inch,
 APPLICANT:
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                                                                                                              180 VNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ 220
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                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                   VNNSEEKDVPKMYCGADGEWLVPIGNCLCNAGHEERSGECQ 274
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Goeddel,
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Wood, William I
Genentech, Inc
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David
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Pred. No. 5.2e-90;
0; Mismatches 28;
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APPLICATION NUMBER: 08/22616

FILING DATE: 04-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Wendy M. Lee

REGISTRATION NUMBER: 00,000

REFERENCE/DOCKET NUMBER: 821P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1994

TELEPAX: 415/225-981

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 36:

GEOIFMAN CHARACTERISTICS: 36:
   GENERAL INFORMATION:
APPLICANT: ZHOU, R
APPLICANT: T.; KRO
APPLICANT: GEORGE,
TITLE OF INVENTION:
                                                                                        Sequence 2, Application Patent No. 5814479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION MINISTER
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APPLICANT:
APPLICANT:
APPLICANT:
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LENGTH: 1104 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST ANTIBODIES NUMBER OF SEQUENCES: 45
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STATE: California
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                                                                                                                                                                                                                                                                                                                                                            VLGTCKETFNLYYMESDDDHGVKFREHQFTKIDTIAADESFTQMDLGDRILKLNTEIREV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                    WEEISGVDEHYTPIRTYQVCNVMDHSQNNWLRTNWVPRNSAQKIYVELKFTLRDCNSIPL 60
                                                                                                                                                                                               VNNSEEKDVPKMYCGADGEWLVPIGNCLCNAGHEERSGECQ
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                                                                                                                                                                                                                                                                                                                                                                                                             WEEVSIMDEKNTPIRTYQVCNVMEPSQNNWLRTDWITREGAQRVYIEIKFTLRDCNSLPG 113
                                                                                                                                                                                                                                                                     GPLSKKGFYLAFQDVGACIALVSVRVFYKKCPLTVRNLAQFPDTITGADTSSLVEVRGSC
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f: ZHOU, RENPING; SCHULZ, NICHOLAS,
f: T.; KROMER, LAWRENCE, F.; VANDE WOUDE,
f: GEORGE, F.
INVENTION: BSK RECEPTOR LIKE
                                                                                                          Application US/08673789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1104 amino acids
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Wood, William I
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Goeddel, David
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Matthews, William
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73.3%;
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Pred. No. 5.2e-90;
30; Mismatches 28
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Search completed: May
Job time: 4147 sec
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; TYPE: AMINO ACID
; STRANDEDNESS: UNKI
; TOPOLOGY: UNKNOWN
US-08-673-789-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: TYROSINE KINASE AND L.
TITLE OF INVENTION: USE IN DIAGNOSTIC AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STRET: 345 PARK AVENUE
CITY: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION NOTA:
APPLICATION NUMBER: US/08/673,789
FILING DATE: 04-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAROL M. GRUPPI
REGISTRATION UNMBER: 37,341
REFERENCE/DOCKET NUMBER: 2026-4105
TELEPAN: (212) 758-4800
TELEPAN: (212) 751-6849
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 877
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                                                                                    180 VNNSKEEDPPRMYCSTEGEWLVPIGKCSCNAGYEERGFMCQ 220
||:| :||:|:|| |||||||||| |||||: ||
265 VNHSVTDDPPKMHCSAEGEWLVPIGKCMCKAGYEEKNGTCQ 305
                                                                                                                                                                                                                                 205 GPLSKKGFYLAFQDVGACIALVSVRVYYKKCPSVVRHLAIFPDTITGADSSQLLEVSGSC 264
                                                                                                                                                                                 121 GPVNKKGFYLAFQDVGACVALVSVRVYFKKCPFTVKNLAMFPDTVP-MDSQSLVEVRGSC 179
                                                                                                                                                                                                                                                                                                       UNKNOWN
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               2000, 22:25:58
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